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(54) Title: A RECOMBINANT ENZYME WITH MUTANASE ACTIVITY

(57) Abstract

The present invention relates to method for constructing an expression vector comprising a mutanase gene obtained from a filamentous fungus suitable for heterologous production comprising the steps of a) isolating a DNA sequence encoding a mutanase from a filamentous fungus, b) introducing a kex2-site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the mutanase, c) cloning the DNA sequence obtained in step b) into a suitable expression vector. The invention also relates to a recombinant expression vector comprising said mutanase gene sequence and a kex2 cleavage site between the DNA sequence encoding the pro-peptide and the region encoding the mature mutanase, a filamentous fungus host cell, a process for producing recombinant mutanase and a recombinant mutanase. It is also the object of the invention to provide compositions useful in oral care products for humans and animals.

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Title: A recombinant enzyme with mutanase activity

FIELD OF THE INVENTION

The present invention relates to a method for constructing an expression vector comprising a mutanase gene obtained from a filamentous fungus suitable for heterologous production, a recombinant expression vector comprising said mutanase gene sequence and a kex2 cleavage site between the DNA sequence encoding the pro-peptide and the DNA sequence encoding the mature mutanase, a filamentous fungus host cell, a process of producing recombinant mutanase, and said recombinant mutanase.

It is also the object of the invention to provide compositions useful in oral care products for humans and animals.

15 BACKGROUND OF THE INVENTION

Mutanases are α -1,3-glucanases (also known as α -1,3-glucanohydrolases) which degrade the α -1,3-glycosidic linkages in mutan. Mutanases have been described from two species of *Trichoderma* (Hasegawa et al., (1969), Journal of Biological Chemistry 244, p. 5460-5470; Guggenheim and Haller, (1972), Journal of Dental Research 51, p. 394-402) and from a strain of *Streptomyces* (Takehara et al., (1981), Journal of Bacteriology 145, p. 729-735), *Cladosporium resinae* (Hare et al. (1978), Carbohydrate Research 66, p. 245-264), *Pseudomonas* sp. (US patent no. 4,438,093), *Flavobacterium* sp. (JP 77038113), *Bacillus circulanse* (JP 63301788) and *Aspergillus* sp.. A mutanase gene from *Trichoderma harzianum* has been cloned and sequenced (Japanese Patent No. 4-58889-A from Nissin Shokuhin Kaisha LTD).

Although mutanases have commercial potential for use as an antiplaque agent in dental applications and personal care products, e.g., toothpaste, chewing gum, or other oral and dental care products, the art has been unable to produce mutanases in significant quantities to be commercial useful.

US patent no. 4,353,891 (Guggenheim et al.) concerns plaque removal using mutanase produced by *Trichoderma harzianum* CBS 243.71 to degrade mutan synthesized by cultivating *Streptococcus*

mutans strain CBS 350.71 identifiable as OMZ 176.

It is an object of the present invention to provide a recombinant mutanase from *Trichoderma harzianum* which can be produced in commercially useful quantities.

5

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 shows plasmid pMT1796

Figure 2 shows plasmid construction of plasmids pMT1796, pMT1802, and pMT1815,

10 Figure 3 shows an outline of the construction of the *A. oryzae* recombinant mutanase expression vector pMT1802,

Figure 4 shows the pH-profile of recombinant and wild-type *T. harzianum* CBS 243.71 mutanase

15 Figure 5 shows the temperature profile of recombinant and wild-type *T. harzianum* CBS 243.71 mutanase at pH 7,

Figure 6 shows the temperature stability of recombinant and wild-type *T. harzianum* CBS 243.71 mutanase at pH 7,

20 Figure 7 shows the indirect Malthus standard curve for a mix culture of *S. mutans*, *A. viscosus* and *F. nucleatum* grown in BHI at 37°C.

SUMMARY OF THE INVENTION

The object of the invention is to provide a recombinant mutanase derived from a filamentous fungus by heterologous 25 expression.

The present inventors have as the first been able to express the mutanase gene of a filamentous fungus heterologously and thus cleared the way for providing a single component, recombinant mutanase essentially free of any contaminants.

30 In the first aspect the invention relates to a method for constructing an expression vector comprising a mutanase gene obtained from a filamentous fungus suitable for heterologous production comprising the steps of:

- a) isolating a DNA sequence encoding a mutanase from a 35 filamentous fungus,
- b) introducing a kex2 site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the

mutanase, or replacing the mutanase (pre)pro-sequence with a (pre)pro-sequence comprising a kex2 or kex2-like site of another fungal enzyme,

5 c) cloning the DNA sequence obtained in step b) into a suitable expression vector.

In a preferred embodiment the mutanase is obtained from a strain within the genus *Trichoderma*.

In step b) the mutanase (pre)pro-sequence may for instance be replaced with the Lipolase® (pre)pro-sequence or the TAKA-10 amylase (pre)pro-sequence.

It is also an object of the invention to provide an expression vector comprising a mutanase gene and a DNA sequence encoding a (pre)pro-peptide with a kex2 site or kex2-like site between the DNA sequences encoding said (pre)pro-peptide and 15 the mature region of the mutanase.

The invention also relates to a filamentous host cell for production of recombinant mutanase derived from a filamentous fungus. Preferred host cells include filamentous fungi of the genera *Trichoderma*, *Aspergillus*, and *Fusarium*.

20 Further, the invention relates to a process for producing a recombinant mutanase in a host cell, comprising the steps:

a) transforming an expression vector comprising a mutanase gene with a kex2 site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the mutanase 25 into a suitable filamentous fungus host cell,

b) cultivating the host cell in a suitable culture medium under conditions permitting expression and secretion of an active mutanase,

c) recovering and optionally purifying the secreted active recombinant mutanase from the culture medium.

The expression vector may be prepared according to the above described method of the invention.

A recombinant mutanase may according to the invention be produced according to the process of the invention.

35 A substantially pure wild-type mutanase obtained from *Trichoderma harzianum* CBS 243.71 essentially free of any contaminants is also part of the invention.

The invention also relates to a composition comprising a recombinant mutanase of the invention or a substantially pure mutanase of the invention useful in oral care products and food, feed and/or pet food products.

5 Finally the invention relates to the use of the recombinant mutanase of the invention or the substantially purified mutanase of the invention or composition or product of the invention preventing the formation of human or animal dental plaque or removing dental plaque and for the use in food, feed and/or pet
10 food products.

DETAILED DESCRIPTION OF THE INVENTION

The object of the invention is to provide a recombinant mutanase derived from a filamentous fungus by heterologous
15 expression.

The present inventors have as the first been able to express the mutanase gene of a filamentous fungus heterologously and thus cleared the way for providing a single component recombinant mutanase essentially free of any contaminants.

20 The principle of the invention can be used for all mutanases derivable from filamentous fungi, such as from filamentous fungi of the genus *Trichoderma*, such a strain of *Trichoderma harzianum*, especially *Trichoderma harzianum* CBS 243.71, and the genera *Streptomyces*, *Cladosporium* or *Aspergillus*.

25 Previously it has not been possible to produce mutanases of filamentous fungi heterologously. Consequently, according to prior art mutanases are produced homologously and comprise a mixture of other enzyme activities besides the mutanase (i.e. with undesired contaminants).

30 An example of this is *Trichoderma harzianum* CBS 243.71 which are known to produce a mutanase as also described above. The mutanase derived from *Trichoderma harzianum* CBS 243.71 has before the successful findings of the present invention only been produced homologously.

35 It is advantageous to be able to produce the mutanase heterologously, as it is then possible to provide a single component mutanase free of undesired contaminants. Further, it

facilitates providing an isolated and purified enzyme of the invention in industrial scale.

According to the invention it is possible to express mutanases derived from filamentous fungi in a suitable host 5 cell by introducing a kex2 cleavage site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature mutanase, or replacing the mutanase (pre)pro-sequence with a (pre)pro-sequence comprising a kex2 site or kex2-like site of another fungal enzyme.

10 The (pre)pro-sequence have for instance be the Lipolase® (pre)pro-sequence or the TAKA-amylase (pre)pro-sequence.

Pro-peptides

A large number of mature proteins are initially synthesised 15 with a N-terminal extension, the pro-peptide, varying from very small peptides (e.g. GLA 6 amino acids) to relatively long peptides (e.g. PEPA 49 amino acids).

The pro-peptide can perform a number of different functions. Firstly, pro-peptides might contribute to the efficiency of co- 20 translational translocation of the protein across the ER-membrane. Secondly, pro-peptides might contribute to co-translational proteolytic processing of the polypeptide. Thirdly, they might act as intracellular targeting signal for routing to specific cellular compartments. Fourthly, in some pro-proteins 25 the pro-peptide keeps the protein inactive until it reaches its site of action.

Removal of the pro-peptide from the mature protein occurs in general by processing by a specific endopeptidase, usually after the two positively charged amino acid residues Arg-Arg, 30 Arg-Lys or Lys-Arg. However, also other amino acid combinations, containing at least one basic amino acid, have been found to be processed.

The absence of these doublets in mature, endogenous secreted proteins might protect them from proteolytic cleavage. As di- 35 basic cleavage is thought to occur in the Golgi, the internal di-basic peptide sequences in cytoplasmic proteins will not be attacked by this processing.

Kex2 sites

Kex2 sites (see e.g. Methods in Enzymology Vol 185, ed. D. Goeddel, Academic Press Inc. (1990), San Diego, CA, "Gene Expression Technology") and kex2-like sites are di-basic recognition sites (i.e. cleavage sites) found between the pro-peptide encoding region and the mature region of some proteins.

Insertion of a kex2 site or a kex2-like site have in certain cases been shown to improve correct endopeptidase processing at 10 the pro-peptide cleavage site resulting in increased protein secretion levels.

However, in a number of other cases insertion of a Kex2 cleavage site did not increase the secretion level. For instance, Cullen et al., (1987), Bio/Technology, vol. 5, p. 15 369-376, found that insertion of a kex2 site in the secretion signal of chymosin (i.e. signal peptide and pro-peptide), which encoded the glucoamylase signal peptide and pro-peptide fused to prochymosin, did not increase the secretion level of recombinant chymosin expressed in a *Aspergillus nidulans* host 20 cell.

Other examples of references showing that insertion of a kex2 site or a kex2-like site do not always increase the secretion level include Valverde et al., (1995), J. of Biolog. Chem, p. 15821-15826)

25 In the context of the present invention the term "heterologous" production means expression of a recombinant enzyme in an host organism different from the original donor organism or expression of a recombinant enzyme by the donor organism.

30 The term "homologous" production means expression of the wild-type enzyme by the original organism.

In the first aspect the invention relates to a method for construction of an expression vector comprising a mutanase gene suitable for heterologous production comprising the steps of:

35 a) isolating a DNA sequence encoding a mutanase from a filamentous fungus known to produce a mutanase,

- b) introducing a kex2 site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the mutanase, or replacing the mutanase (pre)pro-sequence with a (pre)pro-sequence comprising a kex2 or kex2-like site of 5 another fungal enzyme,
- c) cloning the mutanase gene with the kex2 site or kex2-like site obtained in step b) into a suitable expression vector.

In a preferred embodiment of the mutanase gene is obtained from the genus *Trichoderma*, preferably a strain of the species 10 *T. harzianum*, especially the strain *T. harzianum* CBS 243.71.

The complete mutanase gene DNA sequence derived from *Trichoderma harzianum* CBS 243.71 is shown in SEQ ID No. 1

In step b) the mutanase (pre)pro-sequence may for instance be replaced with the Lipolase® (pre)pro-sequence or the TAKA-15 amylase (pre)pro-sequence.

In the examples below illustrating the present invention a kex2-site is inserted into the *Trichoderma harzianum* mutanase gene presented in SEQ ID No. 1 as the site specific mutation E36 → K36.

20

Isolation of the mutanase gene

The DNA sequence encoding a mutanase may, in accordance with well-known procedures, conveniently be isolated from DNA from a suitable source, such as any of the above mentioned organisms 25 known to comprise a mutanase gene, by use of synthetic oligonucleotide probes prepared on the basis of the DNA sequence disclosed herein.

For instance, a suitable oligonucleotide probe may be prepared on the basis of the nucleotide sequences shown in SEQ ID 30 no. 1 or the amino acid sequence shown in SEQ ID no. 2 or any suitable sub-sequence thereof.

According to this method primers are designed from the knowledge to at least a part of SEQ ID No. 2. Fragments of mutanase gene are then PCR amplified by the use of these 35 primers. These fragments are used as probes for cloning the complete gene.

Alternatively, the DNA sequence encoding a mutanase may be isolated by a general method involving

- cloning, in suitable vectors, a DNA or cDNA library from a strain of genus *Trichoderma*,
- 5 - transforming suitable host cells with said vectors,
- culturing the host cells under suitable conditions to express any enzyme of interest encoded by a clone in the DNA library,
- screening for positive clones by determining any mutanase
- 10 activity of the enzyme produced by such clones, and
- isolating the DNA coding an enzyme from such clones.

The general method is further disclosed in WO 93/11249 the contents of which are hereby incorporated by reference.

15 Expression vector

In another aspect the invention relates to an expression vector comprising a mutanase gene and a DNA sequence encoding a pro-peptide with a kex2 site or kex2-like site inserted between the DNA sequences encoding said pro-peptide and the mature 20 region of the mutanase.

In preferred embodiments of the invention the expression vector comprises besides the kex2 site or kex2-like site an operably linked DNA sequence encoding a prepro-peptide (i.e. signal peptide and a pro-peptide). The prepro-sequence may 25 advantageously be the original mutanase signal-sequence or the Lipolase® signal-sequence or the TAKA signal-sequence and the original mutanase pro-sequence or the Lipolase® pro-sequence or the TAKA pro-sequence.

The promoter may be the TAKA promoter or the TAKA:TPI 30 promoter.

In a specific embodiment of the invention the expression vector is the pMT1796 used to illustrate the concept of the invention in Example 3 below.

The choice of vector will often depend on the host cell into 35 which it is to be introduced.

Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the

replication of which is independent of chromosomal replication, e.g. a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into 5 which it has been integrated.

In the vector, the DNA sequence encoding the mutanase should also be operably connected to a suitable promoter and terminator sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and 10 may be derived from genes encoding proteins either homologous or heterologous to the host cell.

The procedures used to ligate the DNA sequences coding for the mutanase, a prepro-sequence including the kex2 site or kex2-like site, the promoter and the terminator, respectively, 15 and to insert them into suitable vectors are well known to persons skilled in the art (cf., for instance, Sambrook et al., (1989), *Molecular Cloning. A Laboratory Manual*, Cold Spring Harbor, NY).

20 Host Cell

A third aspect of the invention relates to a filamentous fungi host cell for production of recombinant mutanase derived from a filamentous fungus of the genus *Trichoderma*, such as a strain of *T. harzianum*, especially *T. harzianum* CBS 243.71, or 25 the genus *Aspergillus*, such as a strain of *A. oryzae* or *A. niger*, or a strain of the genus *Fusarium*, such as a strain of *Fusarium oxysporum*, *Fusarium graminearum* (in the perfect state named *Gibberella zaeae*, previously *Sphaeria zaeae*, synonym with *Gibberella roseum* and *Gibberella roseum* f. sp. *cerealis*), or 30 *Fusarium sulphureum* (in the perfect state named *Gibberella puricaris*, synonym with *Fusarium trichotheciodes*, *Fusarium bactridioides*, *Fusarium sambucium*, *Fusarium roseum*, and *Fusarium roseum* var. *graminearum*), *Fusarium cerealis* (synonym with *Fusarium crokkwellnse*) or *Fusarium venenatum*. 35 The host cell may advantageously be a *F. graminearum* described in WO 96/00787 (from Novo Nordisk A/S), e.g. the strain deposited as *Fusarium graminearum* ATCC 20334. The strain ATCC

20334 was previously wrongly classified as *Fusarium graminearum* (Yoder, W. and Christianson, L. 1997). RAPD-based and classical taxonomic analyses have now revealed that the true identity of the Quorn fungus, ATCC 20334, is *Fusarium venenatum* Nirenburg sp. nov.

In a preferred embodiment of the invention the host cell is a protease deficient or protease minus strain.

This may for instance be the protease deficient strain *Aspergillus oryzae* JaL125 having the alkaline protease gene 10 named "alp" deleted. This strain is described in PCT/DK97/00135 (from Novo Nordisk A/S).

Filamentous fungi cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a 15 manner known per se. The use of *Aspergillus* as a host microorganism is described in EP 238 023 (Novo Nordisk A/S), the contents of which are hereby incorporated by reference.

According to a further aspect the invention relates to a process for producing a recombinant mutanase in a host cell. Said 20 process comprises the following steps:

- a) transforming an expression vector encoding a mutanase gene with a kex2 site or a kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the mutanase into a suitable filamentous fungus host cell,
- 25 b) cultivating the host cell in a suitable culture medium under conditions permitting the expression of the expression vector,
- c) recovering the secreted recombinant mutanase from the culture medium,
- d) and optionally purifying the recombinant mutanase.

30 The recombinant expression vector may advantageously be any of the above described.

Further, the filamentous fungi host cells to be used for production of the recombinant mutanase of the invention according to the process of the invention may be any of the 35 above mentioned host cell, especially of the genera *Aspergillus*, *Fusarium* or *Trichoderma*.

The medium used to culture the transformed host cells may be any conventional medium suitable for growing the host cells in question. The expressed mutanase is secreted into the culture medium and may be recovered from there by well-known procedures including separating the cells from the medium by centrifugation or filtration, precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

10 It is also an important object of the invention to provide a recombinant mutanase produced according to the process of the invention.

The isolated recombinant mutanase has essentially an amino acid sequence as shown in SEQ ID no. 2. From SDS-PAGE a molecular weight around 80 kDa was found.

The pH optimum of the recombinant mutanase was found to lie in the range from 3.5 to 5.5 which equals the pH optimum of the wild-type mutanase (see Figure 4). The temperature optimum of both the recombinant and wild-type mutanase was found to be 20 around 45°C at pH 7 and around 55°C at pH 5.5 (see Figure 5). Further, the residual activity starts to decline at 40°C at pH 7, while the enzyme is more stable at pH 5.5, where the residual activity starts to decline at 55°C.

The inventors have also provided a substantially pure wild-type mutanase obtained from *Trichoderma harzianum* CBS 243.71 essentially free of any active contaminants, such as other enzyme activities.

Composition

30 It is also an object of the invention to provide a composition comprising the recombinant mutanase of the invention or the purified wild-type mutanase essentially free of any active contaminants of the invention.

Oral care composition

In a still further aspect, the present invention relates to an oral care composition useful as an ingredient in oral care products.

An oral care composition of the invention may suitably 5 comprise an amount of the recombinant *Trichoderma harzianum* mutanase equivalent to an enzyme activity, calculated as enzyme activity units in the final oral care product, in the range from 0.001 MU to 1000 MU/ml, preferably from 0.01 MU/ml to 500 MU/ml, such as from 0.1 MU/ml to 100 MU/ml, especially 0.05 MU/ml to 100 10 MU/ml.

It is also contemplated according to the invention to include other enzyme activities than mutanase activity in the oral care composition. Contemplated enzyme activities include activities from the group of enzymes comprising dextranases, 15 oxidases, such as glucose oxidase, L-amino acid oxidase, peroxidases, such as e.g. the *Coprinus* sp. peroxidases described in WO 95/10602 (from Novo Nordisk A/S) or lactoperoxidase or, haloperoxidases, laccases, proteases, such as papain, acidic protease (e.g. the acidic proteases described in WO 95/02044 20 (Novo Nordisk A/S)), endoglucosidases, lipases, amylases, including amyloglucosidases, such as AMG (from Novo Nordisk A/S), and mixtures thereof.

Oral care products

25 The oral care product may have any suitable physical form (i.e. powder, paste, gel, liquid, ointment, tablet etc.). An "oral care product" can be defined as a product which can be used for maintaining or improving the oral hygiene in the mouth of humans and animals, by preventing dental caries, preventing the 30 formation of dental plaque and tartar, removing dental plaque and tartar, preventing and/or treating dental diseases etc.

At least in the context of the present invention oral care products do also encompass products for cleaning dentures, artificial teeth and the like.

35 Examples of such oral care products include toothpaste, dental cream, gel or tooth powder, odontic, mouth washes, pre- or post brushing rinse formulations, chewing gum, lozenges, and candy.

Toothpastes and tooth gels typically include abrasive polishing materials, foaming agents, flavouring agents, humectants, binders, thickeners, sweetening agents, whitening/bleaching/ stain removing agents, water, and optionally 5 enzymes.

Mouth washes, including plaque removing liquids, typically comprise a water/alcohol solution, flavour, humectant, sweetener, foaming agent, colorant, and optionally enzymes.

10 Abrasives

Abrasive polishing material might also be incorporated into the dentifrice product of the invention. According to the invention said abrasive polishing material includes alumina and hydrates thereof, such as alpha alumina trihydrate, magnesium 15 trisilicate, magnesium carbonate, kaolin, aluminosilicates, such as calcined aluminum silicate and aluminum silicate, calcium carbonate, zirconium silicate, and also powdered plastics, such as polyvinyl chloride, polyamides, polymethyl methacrylate, polystyrene, phenol-formaldehyde resins, melamine-formaldehyde 20 resins, urea-formaldehyde resins, epoxy resins, powdered polyethylene, silica xerogels, hydrogels and aerogels and the like. Also suitable as abrasive agents are calcium pyrophosphate, water-insoluble alkali metaphosphates, dicalcium phosphate and/or its dihydrate, dicalcium orthophosphate, 25 tricalcium phosphate, particulate hydroxyapatite and the like. It is also possible to employ mixtures of these substances.

Dependent on the oral care product the abrasive product may be present in from 0 to 70% by weight, preferably from 1% to 70%. For toothpastes the abrasive material content typically lies in 30 the range of from 10% to 70% by weight of the final toothpaste product.

Humectants are employed to prevent loss of water from e.g. toothpastes. Suitable humectants for use in oral care products according to the invention include the following compounds and 35 mixtures thereof: glycerol, polyol, sorbitol, polyethylene glycols (PEG), propylene glycol, 1,3-propanediol, 1,4-butanediol, hydrogenated partially hydrolysed polysaccharides and the like.

Humectants are in general present in from 0% to 80%, preferably 5 to 70% by weight in toothpaste.

Silica, starch, tragacanth gum, xanthan gum, extracts of Irish moss, alginates, pectin, cellulose derivatives, such as 5 hydroxyethyl cellulose, sodium carboxymethyl cellulose and hydroxypropyl cellulose, polyacrylic acid and its salts, polyvinylpyrrolidone, can be mentioned as examples of suitable thickeners and binders, which helps stabilizing the dentifrice product. Thickeners may be present in toothpaste creams and gels 10 in an amount of from 0.1 to 20% by weight, and binders to the extent of from 0.01 to 10% by weight of the final product.

Foaming agents

As foaming agent soap, an-ionic, cat-ionic, non-ionic, amphoteric and/or zwitterionic surfactants can be used. These may be 15 present at levels of from 0% to 15%, preferably from 0.1 to 13%, more preferably from 0.25 to 10% by weight of the final product.

Surfactants

Surfactants are only suitable to the extent that they do not exert an inactivation effect on the present enzymes. Surfactants include fatty alcohol sulphates, salts of sulphonated mono-glycerides or fatty acids having 10 to 20 carbon atoms, fatty acid-albumen condensation products, salts of fatty acids amides 25 and taurines and/or salts of fatty acid esters of isethionic acid.

Sweetening agents

Suitable sweeteners include saccharin.

30

Flavouring agents

Flavours, such as spearmint, are usually present in low amounts, such as from 0.01% to about 5% by weight, especially from 0.1% to 5%.

35

Whitening/bleaching agents

Whitening/bleaching agents include H_2O_2 and may be added in amounts less than 5%, preferably from 0.25 to 4%, calculated on the basis of the weight of the final product.

5 The whitening/bleaching agents may be an enzyme, such as an oxidoreductase. Examples of suitable teeth bleaching enzymes are described in WO 97/06775 (from Novo Nordisk A/S).

Water

10 Water is usually added in an amount giving e.g. toothpaste a flowable form.

Additional agents

Further water-soluble anti-bacterial agents, such as 15 chlorhexidine digluconate, hexetidine, alexidine, quaternary ammonium anti-bacterial compounds and water-soluble sources of certain metal ions such as zinc, copper, silver and stannous (e.g. zinc, copper and stannous chloride, and silver nitrate) may also be included.

20 Also contemplated according to the invention is the addition of compounds which can be used as fluoride source, dyes/colorants, preservatives, vitamins, pH-adjusting agents, anti-caries agents, desensitizing agents etc.

25 Enzymes

Other essential components used in oral care products and in oral care products of the invention are enzymes. Enzymes are biological catalysts of chemical reactions in living systems. Enzymes combine with the substrates on which they act forming an 30 intermediate enzyme-substrate complex. This complex is then converted to a reaction product and a liberated enzyme which continue its specific enzymatic function.

Enzymes provide several benefits when used for cleansing of the oral cavity. Proteases break down salivary proteins, which 35 are adsorbed onto the tooth surface and form the pellicle, the first layer of resulting plaque. Proteases along with lipases destroy bacteria by lysing proteins and lipids which form the

structural components of bacterial cell walls and membranes. Dextranase breaks down the organic skeletal structure produced by bacteria that forms a matrix for bacterial adhesion. Proteases and amylases, not only prevents plaque formation, but also 5 prevents the development of calculus by breaking-up the carbohydrate-protein complex that binds calcium, preventing mineralization.

Toothpaste

10 A toothpaste produced from an oral care composition of the invention (in weight % of the final toothpaste composition) may typically comprise the following ingredients:

Abrasive material	10 to 70%
Humectant	0 to 80%
15 Thickener	0.1 to 20%
Binder	0.01 to 10%
Sweetener	0.1% to 5%
Foaming agent	0 to 15%
Whitener	0 to 5%
20 Enzymes	0.0001% to 20%

In a specific embodiment of the invention the oral care product is toothpaste having a pH in the range from 6.0 to about 8.0 comprising

- a) 10% to 70% Abrasive material
- 25 b) 0 to 80% Humectant
- c) 0.1 to 20% Thickener
- d) 0.01 to 10% Binder
- e) 0.1% to 5% Sweetener
- f) 0 to 15% Foaming agent
- 30 g) 0 to 5% Whitener
- i) 0.0001% to 20% Enzymes.

Said enzymes referred to under i) include the recombinant mutanase of the invention, and optionally other types of enzymes mentioned above known to be used in toothpastes and the like.

Mouth wash

A mouth wash produced from an oral care composition of the invention (in weight % of the final mouth wash composition) may typically comprise the following ingredients:

0-20%	Humectant
0-2%	Surfactant
0-5%	Enzymes
0-20%	Ethanol
10 0-2%	Other ingredients (e.g. flavour, sweetener active ingredients such as fluorides).
0-70%	Water

The mouth wash composition may be buffered with an appropriate buffer e.g. sodium citrate or phosphate in the pH-range 6-7.5.

15 The mouth wash may be in none-diluted form (i.e. must be diluted before use).

Method of Manufacture

The oral care composition and products of the present 20 invention can be made using methods which are common in the oral product area.

According to the present invention the recombinant mutanase and/or the substantially purified mutanase free of active contaminants can be used in food, feed and/or pet food products.

25

MATERIALS AND METHODSMaterialsMicro-organisms

30 *Trichoderma harzianum* CBS 243.71

A. *oryzae* JaL 125: *Aspergillus oryzae* IFO 4177 available from Institute for Fermentation, Osaka; 17-25 Juso Hammachi 2-Chome Yodogawa-ku, Osaka, Japan, having the alkaline protease gene named "alp" (described by Murakami K et al., (1991), Agric. Biol. 35 Chem. 55, p. 2807-2811) deleted by a one step gene replacement method (described by G. May in "Applied Molecular Genetics of Filamentous Fungi" (1992), p. 1-25. Eds. J. R. Kinghorn and G.

Turner; Blackie Academic and Professional), using the *A. oryzae* *pyrG* gene as marker.

E. coli DH5 α

5 Plasmids and Vectors:

pMT1796 (Figure 1 and Figure 2)

pMT1802 (Figure 2)

pMT1815 (Figure 2)

10 pHd414: *Aspergillus* expression vector is a derivative of the plasmid p775 (described in EP 238.023). The construction of the pHd414 is further described in WO 93/11249. pHd414 contains the *A. niger* glucoamylase terminator and the *A. oryzae* TAKA amylase promoter.

pHD414+mut (Figure 3)

15 pHan37 containing the TAKA:TPI promoter

Linkers:

Linker #1:

20 GATCCTCAC A ATG TTG GGC GTT GTC CGC CGT CTA GGC CTA GG
GAGTGT TAC AAC CCG CAA CAG GCT GCA GAT CCG GAT CCG C
Met Leu Gly Val Val Arg Arg Leu Gly Leu Gly

Linker #2:

25 C CAA TAC TGT TAG T
GT ACG GTT ATG ACA ATC AGATC
Ala Cys Gln Tyr Cys ***

Primers:

Primer 1: 5' GGGGGGATCCACCATGAG 3' (SEQ ID No. 3)

30 Primer 2: 5' ACGGTCAGCAGAAGAAGCTCGACGAATAGGACTGGC 3' (SEQ ID No. 4)

Primer 3: 5' GCCAGTCCTATTCGTCGAGCTTCTGCTGACCGT 3' (SEQ ID No. 5)

Primer 4: 5' CCACGGTCACCAACAATAC 3' (SEQ ID No. 6)

35 Primer 5: GGGGGGATCCACCATGAG (SEQ ID No. 7),

Primer 6: ACGGTCAGCAGAAGAAGCTCGACGAATAGGACTGGC (SEQ ID No. 8)

Primer 7: GCCAGTCCTATTCGTCGAGCTTCTGCTGACCGT (SEQ ID NO. 9),

Primer 8: CCACGGTCACCAACAATAC (SEQ ID No. 10).

Enzymes:

lysyl-specific protease from *Achromobacter*

Trichoderma harzianum CBS 243.71 fermentation broth (Batch no. 5 PPM 3897)

Media, Substrates and Solutions:

YPM: 2% maltose, 1% bactopeptone and 0.5% yeast extract)

DAPI: 4',6-diamidino-2-phenylindole (Sigma D-9542)

10 Britton-Robinson Buffer

BHI: Brain Heart Infusion broth

Equipment:

10 kDa cut-off ultra-filtration cassette (Alpha Minisette from 15 Filtron).

Phenyl-sepharose FF (high sub) column (Pharmacia)

Seitz EK1 filter plate

Q-sepharose FF column (Pharmacia)

Applied Biosystems 473A protein sequencer

20 2 litre Kieler fermenter

Olympus model BX50 microscope

Malthus Flexi M2060 (Malthus Instrument Limited)

Methods:

25 **Molecular biology procedures**

All molecular biology procedures including restriction digests, DNA ligations, *E. coli* transformations, DNA isolations, Southern hybridizations, PCR amplifications, and library constructions and screenings were completed using standard techniques (Sambrook, J., Fritsch, E. F., and Maniatis, T. 1989. *Molecular cloning: A laboratory manual*/E.F. Cold Spring Harbor Laboratory Press, Plainview, NY).

Preparation of Mutan

35 Mutan is prepared by growing *Streptococcus mutans* CBS 350.71 at pH 6.5, 37°C (kept constant), and with an aeration rate of 75 rpm in a medium comprised of the following components:

	NZ-Case	6.5 g/litre
	Yeast Extract	6 g/litre
	$(\text{NH}_4)_2\text{SO}_4$	20 g/litre
	K_2PO_4	3 g/litre
5	Glucose	50 g/litre
	Pluronic PE6100	0.1%

After 35 hours, sucrose is added to a final concentration of 60 g/litre to induce glucosyltransferase. The total fermentation time is 75 hours. The supernatant from the fermentation is 10 centrifuged and filtered (sterile). Sucrose is then added to the supernatant to a final concentration of 5% (pH is adjusted to pH 7.0 with acetic acid) and the solution is stirred overnight at 37°C. The solution is filtered and the insoluble mutan is harvested on propex and washed extensively with deionized water 15 containing 1% sodium benzoate, pH 5 (adjusted with acetic acid). Finally, the insoluble mutan is lyophilized and ground.

Determination of mutanase activity (MU)

One Mutanase Unit (MU) is the amount of enzyme which under 20 standard conditions liberates 1 μmol reducing sugar (calculated as glucose) per minute. Reducing sugars were measured with alkaline $\text{K}_3\text{Fe}(\text{CN})_6$.

Standard Conditions

Substrate.....1.5% mutan
25 Reaction time.....15 minutes

Temperature.....40°C

pH.....5.5

A detailed description of Novo Nordisk's analytical method (AF 180/1-GB) is available from Novo Nordisk A/S on request.

30

Mutanase Plate Assay

A 5% mutan suspension is made in 50 mM sodium acetate, pH 5.5 and the suspension is homogenised for 15 minutes in an Ultra Turrax T25 homogenizer at 4°C. 1% agarose in 50 mM sodium 35 acetate, pH 5.5 is made 0.2% with respect to mutan and 12.5 ml agarose is casted in each petri dish (d=10 cm). The sample to be

analyzed for mutanase activity is applied in sample wells punched in the agarose, and the plate is incubated overnight at 37°C, whereafter clearing zones are formed around mutanase containing samples.

5

Western hybridization

Western hybridizations are performed using the ECL western blotting system (Amersham International, plc, Buckinghamshire, England) and a primary antibody solution containing polyclonal 10 rabbit-anti-mutanase. The limit of detection is 0.001 MU/ml.

Mass spectrometry

Mass spectrometry of purified wild-type mutanase is done using matrix assisted laser desorption ionization time-of-flight mass 15 spectrometry in a VG Analytical TofSpec. For mass spectrometry 2 ml of sample is mixed with 2 ml saturated matrix solution (a-cyano-4-hydroxycinnamic acid in 0.1% TFA:acetonitrile (70:30)) and 2 ml of the mixture spotted onto the target plate. Before introduction into the mass spectrometer the solvent is removed by 20 evaporation. Samples are desorbed and ionized by 4 ns laser pulses (337 nm) at threshold laser power and accelerated into the field-free flight tube by an accelerating voltage of 25 kV. Ions are detected by a microchannel plate set at 1850 V.

25 Preparation of Hydroxyapatite disks (HA)

Hydroxyapatite tablets are prepared by compressing 250 mg of hydroxyapatite in a tablet die at about 5,900 kg (13,000 lbs) of pressure for 5 minutes. The tablets are then sintered at 600°C for 4 hours and finally hydrated with sterile deionized water.

30

Plaque coating of Hydroxyapatite disks (HA)

Hydroxyapatite disks (HA) were dry sterilised (121°C, 2 bar, 20 minutes) and coated with filter sterilised saliva for 18 hours at 37°C. The HA disks were placed in a sterile rack in a beaker, 35 Brain Heart Infusion broth (BHI) containing 0.2% sucrose was poured into the beaker covering the disks. Sterile Na₂S (pH 7.0) was added immediately before inoculation given the final concen-

tration of 5 g/litre. A mixture 1:1:1 of *Streptococcus mutans*, *Actinomyces viscosus* and *Fusobacterium nucleatum* grown anaerobically (BHI, 37°C, 24 h) was used as inoculum in the concentration of approximately 10⁶ cfu/ml. The disks were incubated 5 anaerobic at 37°C for 4 days with slight stirring.

Malthus-method for plaque

The Malthus-method is based on the methods described in Johnston et al., (1995), Journal of Microbiological Methods 21, 10 p. 15-26 and Johansen et al. (1995), Journal of Applied Bacteriology 78, p. 297-303.

EXAMPLES

15 Example 1

Purification of wild-type Mutanase

100 g fermentation broth of *Trichoderma harzianum* CBS 243.71 (Batch no. PPM 3897) were dissolved in 1 litre 10 mM sodium acetate, pH 5.2 overnight at 4°C.

20 65 g DEAE-Sephadex A-50 were swelled in 3 litre 10 mM sodium acetate, pH 5.2. Excess buffer was removed after swelling. DEAE-Sephadex was mixed with the crude mutanase preparation for 1 hour and unbound material was collected by filtration through Propex cloth. The gel was further washed with 2.5 l of 10 mM sodium acetate, pH 5.2. A pool containing the unbound material was made; 25 volume 4 litre. Remaining DEAE-Sephadex particles were removed by filtration through a Whatman GF/F filter.

350 ml S-Sepharose was equilibrated in 10 mM sodium acetate, pH 5.2 and mixed with 600 ml of the pool from the DEAE-Sephadex 30 for 10 minutes. Unbound material was collected by filtration through Propex cloth and the gel was washed with 500 ml 10 mM sodium acetate buffer, pH 5.2. Bound material was eluted with the same buffer containing 1 M NaCl. The procedure was repeated 7 times. The combined pool containing the unbound material (7 35 litre) was concentrated on a Filtron concentrator equipped with a 10 kDa cut-off membrane and followed by a buffer change to 10 mM sodium acetate, pH 4.7. The concentrate was filtrated through a

Whatmann GF/F filter. The final volume of the concentrate was 600 ml.

An S-Sepharose column (180 ml, 2.6 x 33 cm) was equilibrated with 10 mM sodium acetate, pH 4.7. The pH adjusted concentrate from the S-Sepharose batch ion exchange was applied onto the column in 50 ml portions with a flow of 10 ml/min. The mutanase was eluted with a linear gradient from 0 to 20 mM NaCl in 3 column volumes. The residual protein was eluted with the same buffer containing 1 M NaCl. Fractions were analyzed for mutanase activity (plate assay) and fractions with high activity were pooled. The procedure was repeated 12 times. The combined mutanase pool was concentrated in a Filtron concentrator equipped with a 10 kDa cut-off membrane and followed by a buffer change to 10 mM Tris-HCl, pH 8.0. The final volume of the concentrate was 15 870 ml.

The concentrated pool from the S-Sepharose column was further purified on a HiLoad Q-Sepharose column (50 ml, 2.6 x 10 cm) equilibrated with 10 mM Tris-HCl, pH 8.0. Portions of 130 ml was applied with a flow of 8 ml/min. Elution of the mutanase was performed with a linear gradient from 0 to 50 mM NaCl in 12 column volumes. Fractions with high mutanase activity (plate assay) were pooled, concentrated in an Amicon cell equipped with a 10 kDa cut-off membrane. Finally, the mutanase preparation was dialyzed extensively against 10 mM sodium phosphate, pH 7.0 and filtrated 25 through a 0.45 mm filter.

The yield of the mutanase in the purification described above was 300 mg. The purity of the HiLoad-Q preparation was analyzed by SDS-PAGE and N-terminal sequencing and judged by both methods the purity was around 95%.

30

Example 2

N-terminal sequencing of wild-type Mutanase

N-terminal amino acid sequencing was carried out in an Applied Biosystems 473A protein sequencer.

35 To generate peptides reduced and S-carboxymethylated mutanase (» 450 mg) was digested with the lysyl-specific protease from *Achromobacter* (10 mg) in 20 mM NH₄HCO₃ for 16 hours at 37°C. The

resulting peptides were separated by reversed phase HPLC using a Vydac C₁₈ column eluted with a linear gradient of 80% 2-propanol containing 0.08% TFA in 0.1% aqueous TFA. Peptides were repurified by reversed-phase-HPLC using a Vydac C₁₈ column eluted with linear gradients of 80% acetonitrile containing 0.08% TFA in 0.1% aqueous TFA before being subjected to N-terminal amino acid sequencing.

The amino acid sequences determined are given below.

N-terminal:

10 Ala-Ser-Ser-Ala-Asp-Arg-Leu-Val-Phe-Cys-His-Phe-Met-Ile-Gly-Ile-
Val-Gly-Asp-Arg-Gly-Ser-Ser-Ala-Asp-Tyr-Asp-Asp-Asp-
Peptide 1:

Val Phe-Ile-Ser-Phe-Asp-Phe-Asn-Trp-Trp-Ser-Pro-Gly-Asn-Ala-Val-
Gly-Val-Gly-Gln-Lys

15 Peptide 2:

Pro-Tyr-Leu-Ala-Pro-Val-Ser-Pro-Trp-Phe-Phe-Thr-His-Phe-Gly-Pro-
Glu-Val-Ser-Tyr-Ser-

Peptide 3:

Trp-Val-Asn-Asp-Met-Pro-His-Asp-Gly-Phe-Leu-Asp-Leu-Ser-Lys

20

Example 3

Construction of the mutanase expression vectors, pMT1796, pMT1802 and pMT1815

A CDNA clone encoding mutanase was identified in a 25 *Trichoderma harzianum* CBS 243.71 library by hybridization with a fragment of the gene amplified by PCR using primers based on the mutanase sequence shown in SEQ ID NO. 1.

DNA sequence analysis of the isolated clone, pHd414+mut, showed that it indeed encoded the mutanase gene, and that the 30 5' end of the construct contained a long leader sequence. To remove this leader, pHd414+mut was restricted with the enzymes EcoRI, NarI and XhoI. From this digestion a 3499 nt (nucleotide) vector fragment and a 610 nt NarI/XhoI fragment were isolated. These two fragments were then ligated with 35 linker #1 (see above) and a 618 nt EcoRI/BamHI fragment from pHan37 containing the TAKA:TPI promoter, giving plasmid pJW99. HD414+mut was next digested with XhoI and SphI, and a 1790 nt

fragment encoding amino acids 35-598 of the mutanase gene was isolated.

This fragment was ligated with linker #2 (see above) and pJW99 that had been linearized with the restriction enzymes 5 *Xba*I and *Xho*I. The resulting plasmid, pMT1802, contains the *T. harzianum* mutanase gene under the control of the TAKA:TPI promoter. Plasmid pMT1796 is identical to pMT1802 except that E36 of the mutanase protein has been changed to K36 by replacing the *Xho*I/*Kpn*I fragment of pMT1802 with a PCR amplified fragment 10 containing the desired mutation.

This PCR fragment was created in a two step procedure as reported in Ho, et al. (1989), Gene, 77, p. 51-59, using the following primers:

Primer 1 (nt 2751 5' CAGCGTCCACATCACGAGC nt 2769) and 15 Primer 2 (nt 3306 5' GAAGAAGCACGTTCTCGAGAGACCG nt 3281);
Primer 3 (nt 3281 5' CGGTCTCTGAGAACGTGCTTCTTC nt 3306) and
Primer 4 (nt 4266 5' GCCACTTCCGTTATTAGCC nt 4248); nucleotide numbers refer to the pMT1802 plasmid (See SEQ ID No. 11).

To create pMT1815, a 127 nt DNA fragment was PCR amplified 20 using again a two step procedure and the primers:

Primer 5: GGGGGGATCCACCATGAG;
Primer 6: ACGGTCAAGCAGAAGAACGCTCGACGAATAGGACTGGC;
Primer 7: GCCAGTCCTATTCTCGAGCTTCTTGCTGACCGT;
Primer 8: CCACGGTCACCAACAAATAC,
25 and the plasmids pHan37 and pMT1802 as templates in the first round of amplification.

This fragment contains a *Bam*HI restriction enzyme site followed by the Lipolase® prepro-sequence in frame with residues 38-54 of the mutanase protein and ending with a *Bst*EII 30 site.

The fragment was digested with the restriction enzymes *Bst*EII and *Bam*HI and inserted into pMT1802 that had been linearized with the same pair of enzymes. Changes in constructs were confirmed and the integrity of the resulting coding 35 regions were checked by nucleotide sequencing.

Example 4**Expression of recombinant Mutanase in *Aspergillus oryzae***

The strain *A. oryzae* JaL125 was transformed using a PEG-mediated protocol (see EP 238 023) and a DNA mixture containing 5 0.5 µg of a plasmid encoding the gene that confers resistance to the herbicide Basta and 8.0 µg of one of the three mutanase expression plasmids. Transformants were selected on minimal plates containing 0.5% basta and 50 mM urea as a nitrogen source.

10

Shake flask cultures

Transformed colonies were spore purified twice on selection media and spores were harvested. A 20 ml universal container (Nunc, cat #364211) containing 10 ml YPM (2% maltose, 1% 15 bactopeptone and 0.5% yeast extract) was inoculated with spores and grown for 5 days with shaking at 30°C. The supernatant was harvested after 5 days growth.

Construct	highest mutanase level detected	number of transformants tested
pMT1802, mutanase prepro + mutanase	<0.001	10
pMT1796, mutanase prepro + KEX2 + mutanase	3.8	4
pMT1815, Lipolase® prepro + mutanase	0.16	22

Table 1 Comparison of mutanase expression from the three different 20 expression constructs. The limit of detection was 0.001 MU/ml

The presence of mutanase in culture supernatants was examined by western hybridizations. SDS-PAGE and protein transfers were performed using standard protocols.

25

Example 5**Purification of recombinant mutanase**

700 ml fermentation broth was filtered and concentrated. The pH was adjusted to 4.7 (conductivity around 300 µS/cm) and the 30 broth was loaded onto an S-Sepharose column (XK 50/22) (Pharmacia) equilibrated in 10 mM sodium acetate pH 4.7. The

mutanase was eluted in a linear NaCl gradient. The major part of the mutanase appeared in the unbound fractions. These fractions were pooled and concentrated. Then the concentrate was loaded onto a HiLoad Q-Sepharose column (Pharmacia) 5 equilibrated in 10 mM Tris-HCl, pH 8.0 (around 600 μ S/cm). The mutanase was eluted in a linear gradient of NaCl and the mutanase containing-fractions were pooled according to purity and activity. The pooled fractions were concentrated and a fraction was further purified by gelfiltration on a Superdex 75 10 (16/60) column (Pharmacia) in sodium acetate pH 6.0.

The purified mutanase has a specific activity around 19 MU pr. absorption unit at 280 nm. From SDS-PAGE (Novex 4-20 %; run according to the manufacturer's instructions) a molecular weight around 80 kDa is found.

15 The N-terminal amino acid sequence was confirmed to be identical to the N-terminal amino acid sequence of the wt mutanase (Ala-Ser-Ser-Ala-) (see Example 2)

Example 6

20 pH-profile of mutanase

500 ml 5 % mutan in 50 mM Britton-Robinson buffer at varying pH was added 2 ml enzyme sample (diluted in MilliQ-filtered water) in large vials (to ensure sufficient agitation) and incubated for 15 minutes at 40°C while shaking vigorously. The 25 reaction was terminated by adding 0.5 ml 0.4 M NaOH and the samples were filtered on Munktell filters. 100 μ l filtrate in Eppendorf vials were added 750 μ l ferricyanide reagent (0.4 g/l $K_3Fe(CN)_6$, 20 g/l Na_2CO_3) and incubated 15 minutes at 85°C. After allowing the samples to cool, the decrease in absorption 30 at 420 nm was measured. A dilution series of glucose was included as a standard. Substrate and enzyme blanks were always included. Samples were run in duplicate. The pH-optimum for both wild-type and recombinant enzyme is around pH 3.5-5.5 (see Figure 4).

35

Example 7

Temperature profile of mutanase:

500 ml 5 % mutan in 100 mM sodium acetate, pH 5.5 or in 100 mM sodium phosphate, pH 7 was added 2 ml enzyme sample (diluted in MilliQ-filtered water) in large vials (to ensure sufficient 5 agitation) and incubated for 15 minutes at various temperatures while shaking vigorously. The reaction was terminated by adding 0.5 ml 0.4 M NaOH and the samples were filtered on Munktell filters. 100 μ l filtrate in Eppendorf vials were added 750 μ l ferricyanide reagent (0.4 g/l $K_3Fe(CN)_6$, 20 g/l Na_2CO_3) and in-10 cubated 15 minutes at 85°C. After allowing the samples to cool, the drop in absorption at 420 nm was measured. A dilution series of glucose was included as a standard. Substrate and enzyme blanks were always included. Samples were run in duplicate. The temperature profiles for the recombinant and wt 15 mutanase were identical. The temperature optimum at pH 7 was around 45 °C. The temperature optimum at pH 5.5 was above 55° (See Figure 5).

Example 8**20 Temperature stability of mutanase:**

The temperature stability was investigated by pre-incubating enzyme samples for 30 minutes at various temperatures in 0.1 M sodium acetate, pH 5.5 or in 0.1 M sodium phosphate, pH 7 before assaying the residual activity. Both recombinant and wt 25 mutanase have similar temperature stability profiles. The residual activity starts to decline at 40 °C at pH 7, while the enzyme is more stable at pH 5.5, where the residual activity starts to decline at 55°C (See Figure 6).

30 Example 9**Molecular weight of purified wild-type Mutanase**

The mass spectrometry, performed as described above, of the mutanase revealed an average mass around 75 kDa. In addition, it was clear from the spectra that the glycosylation of the mutanase 35 is heterogeneous. The peptide mass of the mutanase is more than 64 kDa meaning that more than 11 kDa of carbohydrate is attached

to the enzyme.

Example 10

Activity of mutanase against Dental Plaque

5 A plaque biofilm was grown anaerobic on saliva coated hydroxyapatite disks as described in the Material and Methods Section above. The plaque was a mixed culture of *Streptococcus mutans* (SFAG, CBS 350.71), *Actinomyces viscosus* (DSM 43329) and *Fusobacterium nucleatum* subsp. *polymorphum* (DSM 20482).

10 HA disks with plaque were transferred to acetate buffer (pH 5.5) containing recombinant *Trichoderma* mutanase 1 MU/ml and whirled for 2 minutes (sterile buffer was used as control).

After enzyme treatment, the disks were either DAPI stained or transferred to Malthus cells, as indirect impedance measurements 15 were used when enumerating living adherent cells (Malthus Flexi M2060, Malthus Instrument Limited).

For the impedance measurements 3 ml of BHI were transferred to the outer chamber of the indirect Malthus cells, and 0.5 ml of 20 sterile KOH (0.1 M) was transferred to the inner chamber. After mutanase-treatment the disks with plaque were slightly rinsed with phosphate buffer and transferred to the outer chamber. The detection times (dt) in Malthus were converted to colony counts by use of a calibration curve relating cfu/ml to dt (Figure 7).

The calibration curve was constructed by a series of 10-fold 25 dilution rate prepared from the mixed culture. Conductance dt of each dilution step was determined in BHI and a calibration curve relating cfu/ml of the 10 fold dilutions to dt in BHI was constructed for the mixed culture (Figure 7).

The removal of plaque from the disks was also determined by 30 fluorescent microscopy, after mutanase treatment disks were stained with DAPI (3 mM) and incubated in the dark for 5 minutes (20°C). The DAPI stained cells were examined with the x 100 oil immersion fluorescence objective on an Olympus model BX50 microscope equipped with a 200 W mercury lamp and an UV- filter.

35 The result was compared with the quantitative data obtained by the impedance measurements.

The number of living cells on the saliva treated HA-surface after enzyme treatment was determined by the Malthus method and shown in Table 1. However, by the Malthus method it is not possible to distinguish between a bactericidal activity of 5 mutanase or an enzymatic removal of the plaque. Therefore a decrease in living bacteria on the surface has to be compared with the simultaneously removal of plaque from the surface which is estimated by the DAPI staining.

Mutanase (MU/ml)	Log ₁₀ reduction (cfu/cm ²)	Removal of plaque (%)	No. of observations
0	0	0	10
1	1.4	96	6

10 Table 2: Enzymatic plaque removal (pH 5.5, 2 minutes) from saliva treated hydroxyapatite determined by impedance measurements.

A significant removal of plaque was determined by fluorescent microscopy after treatment with mutanase. Thus mutanase reduced 15 the amount of adhering cells. However, the activity was observed as a removal of plaque and not as a bactericidal activity against cells in plaque.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Novo Nordisk A/S
 (B) STREET: Novo Alle
 (C) CITY: Bagsvaerd
 (E) COUNTRY: Denmark
 (F) POSTAL CODE (ZIP): DK-2880
 (G) TELEPHONE: +45 4444 8888
 (H) TELEFAX: +45 4449 3256

(ii) TITLE OF INVENTION: A recombinant enzyme with mutanase activity

(iii) NUMBER OF SEQUENCES: 11

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1905 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: Trichoderma harzianum CBS 243.71

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1905
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG	TTG	GGC	GTT	GTC	CGC	CGT	CTA	GGC	GCC	CTT	GCT	GCC	GCA	48		
Met	Leu	Gly	Val	Val	Arg	Arg	Leu	Gly	Leu	Gly	Ala	Leu	Ala	Ala		
1			5				10				15					
GCT	CTG	TCT	CTC	GGC	AGT	GCC	GCT	CCC	GCC	AAT	GTT	GCT	ATT	CGG	96	
Ala	Leu	Ser	Ser	Leu	Gly	Ser	Ala	Ala	Pro	Ala	Asn	Val	Ala	Ile	Arg	
		20				25					30					
TCT	CTC	GAG	GAA	CGT	GCT	TCT	TCT	GCT	GAC	CGT	CTC	GTA	TTC	TGT	CAC	144
Ser	Leu	Glu	Glu	Arg	Ala	Ser	Ser	Ala	Asp	Arg	Leu	Val	Phe	Cys	His	
		35			40			45								
TTC	ATG	ATT	GGT	ATT	GGT	GAC	CGT	GGC	AGC	TCA	GCA	GAC	TAT	GAT	192	
Phe	Met	Ile	Gly	Ile	Val	Gly	Asp	Arg	Gly	Ser	Ser	Ala	Asp	Tyr	Asp	
		50			55			60								
GAT	GAC	ATG	CAA	CGT	GCC	AAA	GCC	GCT	GGC	ATT	GAC	GCA	TTC	GCT	CTG	240
Asp	Asp	Met	Gln	Arg	Ala	Lys	Ala	Ala	Gly	Ile	Asp	Ala	Phe	Ala	Leu	
		65			70			75			80					
AAC	ATC	GGC	GTT	GAC	GGC	TAT	ACC	GAC	CAG	CAA	CTC	GGG	TAT	GCC	TAT	288
Asn	Ile	Gly	Val	Asp	Gly	Tyr	Thr	Asp	Gln	Gln	Leu	Gly	Tyr	Ala	Tyr	
		85			90			95								
GAC	TCT	GCC	GAC	CGT	AAT	GGC	ATG	AAA	GTC	TTC	ATT	TCA	TTC	GAT	TTC	336
Asp	Ser	Ala	Asp	Arg	Asn	Gly	Met	Lys	Val	Phe	Ile	Ser	Phe	Asp	Phe	
		100			105			110								
AAC	TGG	TGG	AGC	CCC	GGT	AAT	GCA	GTT	GGT	GTT	GGC	CAG	AAG	ATT	GCG	384
Asn	Trp	Trp	Ser	Pro	Gly	Asn	Ala	Val	Gly	Val	Gly	Gln	Lys	Ile	Ala	
		115			120			125								

CAG TAT GCC AGC CGT CCC GCC CAG CTG TAT GTT GAC AAC CGG CCA TTC Gln Tyr Ala Ser Arg Pro Ala Gln Leu Tyr Val Asp Asn Arg Pro Phe 130 135 140	432
GCC TCT TCC TTC GCT GGT GAC GGT TTG GAT GTA AAT GCG TTG CGC TCT Ala Ser Ser Phe Ala Gly Asp Gly Leu Asp Val Asn Ala Leu Arg Ser 145 150 155 160	480
GCT GCA GGC TCC AAC GTT TAC TTT GTG CCC AAC TTC CAC CCT GGT CAA Ala Ala Gly Ser Asn Val Tyr Phe Val Pro Asn Phe His Pro Gly Gln 165 170 175	528
TCT TCC CCC TCC AAC ATT GAT GGC GCC CTC AAC TGG ATG GCC TGG GAT Ser Ser Pro Ser Asn Ile Asp Gly Ala Leu Asn Trp Met Ala Trp Asp 180 185 190	576
AAT GAT GGA AAC AAC AAG GCA CCC AAG CCG GGC CAG ACT GTC ACG GTG Asn Asp Gly Asn Asn Lys Ala Pro Lys Pro Gly Gln Thr Val Thr Val 195 200 205	624
GCA GAC GGT GAC AAC GCT TAC AAG AAT TGG TTG GGT GGC AAG CCT TAC Ala Asp Gly Asp Asn Ala Tyr Lys Asn Trp Leu Gly Gly Lys Pro Tyr 210 215 220	672
CTA GCG CCT GTC TCC CCT TGG TTT TTC ACC CAT TTT GGC CCT GAA GTT Leu Ala Pro Val Ser Pro Trp Phe Phe Thr His Phe Gly Pro Glu Val 225 230 235 240	720
TCA TAT TCC AAG AAC TGG GTC TTC CCA GGT GGT CCT CTG ATC TAT AAC Ser Tyr Ser Lys Asn Trp Val Phe Pro Gly Gly Pro Leu Ile Tyr Asn 245 250 255	768
CGG TGG CAA CAG GTC TTG CAG CAG GGC TTC CCC ATG GTT GAG ATT GTT Arg Trp Gln Gln Val Leu Gln Gln Gly Phe Pro Met Val Glu Ile Val 260 265 270	816
ACC TGG AAT GAC TAC GGC GAG TCT CAC TAC GTC GGT CCT CTG AAG TCT Thr Trp Asn Asp Tyr Gly Glu Ser His Tyr Val Gly Pro Leu Lys Ser 275 280 285	864
AAG CAT TTC GAT GAT GGC AAC TCC AAA TGG GTC AAT GAT ATG CCC CAT Lys His Phe Asp Asp Gly Asn Ser Lys Trp Val Asn Asp Met Pro His 290 295 300	912
GAT GGA TTC TTG GAT CTT TCA AAG CCG TTT ATT GCT GCA TAT AAG AAC Asp Gly Phe Leu Asp Leu Ser Lys Pro Phe Ile Ala Ala Tyr Lys Asn 305 310 315 320	960
AGG GAT ACT GAT ATA TCT AAG TAT GTT CAA AAT GAG CAG CTT GTT TAC Arg Asp Thr Asp Ile Ser Lys Tyr Val Gln Asn Glu Gln Leu Val Tyr 325 330 335	1008
TGG TAC CGC CGC AAC TTG AAG GCA TTG GAC TGC GAC GCC ACC GAC ACC Trp Tyr Arg Arg Asn Leu Lys Ala Leu Asp Cys Asp Ala Thr Asp Thr 340 345 350	1056
ACC TCT AAC CGC CCG GCT AAT AAC GGA AGT GGC AAT TAC TTT ATG GGA Thr Ser Asn Arg Pro Ala Asn Asn Gly Ser Gly Asn Tyr Phe Met Gly 355 360 365	1104
CGC CCT GAT GGT TGG CAA ACT ATG GAT GAT ACC GTT TAT GTT GCC GCA Arg Pro Asp Gly Trp Gln Thr Met Asp Asp Thr Val Tyr Val Ala Ala 370 375 380	1152
CTT CTC AAG ACC GCC GGT AGC GTC ACG GTC ACG TCT GGC GGC ACC ACT Leu Leu Lys Thr Ala Gly Ser Val Thr Val Thr Ser Gly Gly Thr Thr	1200

385	390	395	400	
CAA ACG TTC CAG GCC AAC GCC GGA AAC CTC TTC CAA ATC CCT GCC Gln Thr Phe Gln Ala Asn Ala Gly Ala Asn Leu Phe Gln Ile Pro Ala 405	410	415		1248
AGC ATC GGC CAG CAA AAG TTT GCT CTA ACT CGC AAC GGT CAG ACC GTC Ser Ile Gly Gln Gln Lys Phe Ala Leu Thr Arg Asn Gly Gln Thr Val 420	425	430		1296
TTT AGC GGA ACC TCA TTG ATG GAT ATC ACC AAC GTT TGC TCT TGC GGT Phe Ser Gly Thr Ser Leu Met Asp Ile Thr Asn Val Cys Ser Cys Gly 435	440	445		1344
ATC TAC AAT TTC AAC CCA TAT GTT GGC ACC ATT CCT GCC GGC TTT GAC Ile Tyr Asn Phe Asn Pro Tyr Val Gly Thr Ile Pro Ala Gly Phe Asp 450	455	460		1392
GAC CCT CTT CAG GCT GAC GGT CTT TTC TCT TTG ACC ATC GGA TTG CAT Asp Pro Leu Gln Ala Asp Gly Leu Phe Ser Leu Thr Ile Gly Leu His 465	470	475	480	1440
GTC ACG ACT TGT CAG GCC AAG CCA TCT CTT GGA ACC AAC CCT CCT GTC Val Thr Thr Cys Gln Ala Lys Pro Ser Leu Gly Thr Asn Pro Pro Val 485	490	495		1488
ACT TCT GGC CCT GTG TCC TCG CTG CCA GCT TCC TCC ACC ACC CGC GCA Thr Ser Gly Pro Val Ser Ser Leu Pro Ala Ser Ser Thr Thr Arg Ala 500	505	510		1536
TCC TCG CCT CCT GTT TCT TCA ACT CGT GTC TCT TCT CCC CCT GTC TCT Ser Ser Pro Pro Val Ser Ser Thr Arg Val Ser Ser Pro Pro Val Ser 515	520	525		1584
TCC CCT CCA GTT TCT CGC ACC TCT TCT CCC CCT CCC CCG GCC AGC Ser Pro Pro Val Ser Arg Thr Ser Ser Pro Pro Pro Pro Ala Ser 530	535	540		1632
AGC ACG CCG CCA TCG GGT CAG GTT TGC GTT GCC GGC ACC GTT GCT GAC Ser Thr Pro Pro Ser Gly Gln Val Cys Val Ala Gly Thr Val Ala Asp 545	550	555	560	1680
GGC GAG TCC GGC AAC TAC ATC GGC CTG TGC CAA TTC AGC TGC AAC TAC Gly Glu Ser Gly Asn Tyr Ile Gly Leu Cys Gln Phe Ser Cys Asn Tyr 565	570	575		1728
GGT TAC TGT CCA CCG GGA CCG TGT AAG TGC ACC GCC TTT GGT GCT CCC Gly Tyr Cys Pro Pro Gly Pro Cys Lys Cys Thr Ala Phe Gly Ala Pro 580	585	590		1776
ATC TCG CCA CCG GCA AGC AAT GGG CGC AAC GGC TGC CCT CTA CCG GGA Ile Ser Pro Pro Ala Ser Asn Gly Arg Asn Gly Cys Pro Leu Pro Gly 595	600	605		1824
GAA GGC GAT GGT TAT CTG GGC CTG TGC AGT TTC AGT TGT AAC CAT AAT Glu Gly Asp Gly Tyr Leu Gly Leu Cys Ser Phe Ser Cys Asn His Asn 610	615	620		1872
TAC TGC CCG CCA ACG GCA TGC CAA TAC TGT TAG Tyr Cys Pro Pro Thr Ala Cys Gln Tyr Cys *	630	635		1905

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 635 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Gly Val Val Arg Arg Leu Gly Leu Gly Ala Leu Ala Ala Ala
 1 5 10 15

Ala Leu Ser Ser Leu Gly Ser Ala Ala Pro Ala Asn Val Ala Ile Arg
 20 25 30

Ser Leu Glu Glu Arg Ala Ser Ser Ala Asp Arg Leu Val Phe Cys His
 35 40 45

Phe Met Ile Gly Ile Val Gly Asp Arg Gly Ser Ser Ala Asp Tyr Asp
 50 55 60

Asp Asp Met Gln Arg Ala Lys Ala Ala Gly Ile Asp Ala Phe Ala Leu
 65 70 75 80

Asn Ile Gly Val Asp Gly Tyr Thr Asp Gln Gln Leu Gly Tyr Ala Tyr
 85 90 95

Asp Ser Ala Asp Arg Asn Gly Met Lys Val Phe Ile Ser Phe Asp Phe
 100 105 110

Asn Trp Trp Ser Pro Gly Asn Ala Val Gly Val Gly Gln Lys Ile Ala
 115 120 125

Gln Tyr Ala Ser Arg Pro Ala Gln Leu Tyr Val Asp Asn Arg Pro Phe
 130 135 140

Ala Ser Ser Phe Ala Gly Asp Gly Leu Asp Val Asn Ala Leu Arg Ser
 145 150 155 160

Ala Ala Gly Ser Asn Val Tyr Phe Val Pro Asn Phe His Pro Gly Gln
 165 170 175

Ser Ser Pro Ser Asn Ile Asp Gly Ala Leu Asn Trp Met Ala Trp Asp
 180 185 190

Asn Asp Gly Asn Asn Lys Ala Pro Lys Pro Gly Gln Thr Val Thr Val
 195 200 205

Ala Asp Gly Asp Asn Ala Tyr Lys Asn Trp Leu Gly Gly Lys Pro Tyr
 210 215 220

Leu Ala Pro Val Ser Pro Trp Phe Phe Thr His Phe Gly Pro Glu Val
 225 230 235 240

Ser Tyr Ser Lys Asn Trp Val Phe Pro Gly Gly Pro Leu Ile Tyr Asn
 245 250 255

Arg Trp Gln Gln Val Leu Gln Gln Gly Phe Pro Met Val Glu Ile Val
 260 265 270

Thr Trp Asn Asp Tyr Gly Glu Ser His Tyr Val Gly Pro Leu Lys Ser
 275 280 285

Lys His Phe Asp Asp Gly Asn Ser Lys Trp Val Asn Asp Met Pro His
 290 295 300

Asp Gly Phe Leu Asp Leu Ser Lys Pro Phe Ile Ala Ala Tyr Lys Asn
 305 310 315 320

Arg Asp Thr Asp Ile Ser Lys Tyr Val Gln Asn Glu Gln Leu Val Tyr
 325 330 335

Trp Tyr Arg Arg Asn Leu Lys Ala Leu Asp Cys Asp Ala Thr Asp Thr

340	345	350	
Thr Ser Asn Arg Pro Ala Asn Asn Gly Ser Gly Asn Tyr Phe Met Gly			
355	360	365	
Arg Pro Asp Gly Trp Gln Thr Met Asp Asp Thr Val Tyr Val Ala Ala			
370	375	380	
Leu Leu Lys Thr Ala Gly Ser Val Thr Val Thr Ser Gly Gly Thr Thr			
385	390	395	400
Gln Thr Phe Gln Ala Asn Ala Gly Ala Asn Leu Phe Gln Ile Pro Ala			
405	410	415	
Ser Ile Gly Gln Gln Lys Phe Ala Leu Thr Arg Asn Gly Gln Thr Val			
420	425	430	
Phe Ser Gly Thr Ser Leu Met Asp Ile Thr Asn Val Cys Ser Cys Gly			
435	440	445	
Ile Tyr Asn Phe Asn Pro Tyr Val Gly Thr Ile Pro Ala Gly Phe Asp			
450	455	460	
Asp Pro Leu Gln Ala Asp Gly Leu Phe Ser Leu Thr Ile Gly Leu His			
465	470	475	480
Val Thr Thr Cys Gln Ala Lys Pro Ser Leu Gly Thr Asn Pro Pro Val			
485	490	495	
Thr Ser Gly Pro Val Ser Ser Leu Pro Ala Ser Ser Thr Thr Arg Ala			
500	505	510	
Ser Ser Pro Pro Val Ser Ser Thr Arg Val Ser Ser Pro Pro Val Ser			
515	520	525	
Ser Pro Pro Val Ser Arg Thr Ser Ser Pro Pro Pro Pro Pro Ala Ser			
530	535	540	
Ser Thr Pro Pro Ser Gly Gln Val Cys Val Ala Gly Thr Val Ala Asp			
545	550	555	560
Gly Glu Ser Gly Asn Tyr Ile Gly Leu Cys Gln Phe Ser Cys Asn Tyr			
565	570	575	
Gly Tyr Cys Pro Pro Gly Pro Cys Lys Cys Thr Ala Phe Gly Ala Pro			
580	585	590	
Ile Ser Pro Pro Ala Ser Asn Gly Arg Asn Gly Cys Pro Leu Pro Gly			
595	600	605	
Glu Gly Asp Gly Tyr Leu Gly Leu Cys Ser Phe Ser Cys Asn His Asn			
610	615	620	
Tyr Cys Pro Pro Thr Ala Cys Gln Tyr Cys *			
625	630	635	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer 1"

CAGCGTCCAC ATCACGAGC

19

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer 2"

GAAGAAGCAC GTTTCTGCAG AGACCG

26

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer 3"

CGGTCTCTCG AGAAACGTGC TTCTTC

26

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer 4"

GCCACTTCCG TTATTAGCC

19

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer 5"

GGGGGGATCC ACCATGAG

18

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer 6"

ACGGTCAGCA GAAGAAGCTC GACGAATAGG ACTGGC

36

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer 7"

GCCAGTCCTA TTCTCGAGC TTCTCTGCT GACCGT

36

(2) INFORMATION FOR SEQ ID NO: 10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer 8"

CCACGGTCAC CAACAATAC

19

(2) INFORMATION FOR SEQ ID NO: 11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6032 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (vi) ORIGINAL SOURCE:
 (B) STRAIN: Trichoderma harzianum CBS 243.71
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3188..5092
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCTATGATA ATAATGGTTT	60
CTTAGACGTC AGGTGGCACT TTTCGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT	120
TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAT	180
AATATTGAAA AACAGAGACT ATGAGTATTAC ACACATTCCG TGTCGCCCTT ATTCCCTTTT	240
TTGCGGATT TTGCGCTTC GTTTTGCTC ACCCAGAAC GCTGGTGAAA GTAAAAGATG	300
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAAC GGATCTCAAC AGCGGTAAGA	360
TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC	420
TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC	480
ACTATTCTCA GAATGACTTG GTTGAGTACT CACCACTCAC AGAAAAGCAT CTTACGGATG	540
GCATGACAGT AAGAGAATTAA TGCAGTGCTG CCATAACCAC GAGTGATAAC ACTGCGGCCA	600
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG	660
GGGATCATGT AACTCGCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG	720
ACCGCGTGA CACCAACGATG CCTGTAGCAA TGCCAAACAC GTTGGCGAAA CTATTAACG	780
GCGAACTACT TACTCTAGCT TCCCGGCAAC ATTAATAGA CGGGATGGAG GCGGATAAAAG	840
TTGCAGGGACC ACTTCTGCCTC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	900
GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT	960
CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC	1020
AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT	1080
CATATATACT TTAGATTGAT TAAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA	1140
TCCTTTTGTA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTCGTTT CACTGAGCGT	1200
CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG CGCGTAATCT	1260
GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTGGCC GATCAAGAGC	1320
TACCAACTCT TTTCCGAAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC	1380
TTCTAGTGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC	1440
TCGCTCTGCT AATCCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG	1500
GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGTT	1560
CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG	1620
AGCATTGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CGCGTAAGCG	1680

GCAGGGTCGG	AACAGGAGAG	CCGACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	1740
ATAGTCCTGT	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTGTGA	TGCTCGTCAG	1800
GGGGCGGAG	CCTATGGAAA	AACGCCAGCA	ACGCCGCTT	TTTACGGTTC	CTGGCCTTT	1860
GCTGCCCTT	TGCTCACATG	TTCTTCCGT	CGTTATCCCG	TGATTCGTG	GATAACCGTA	1920
TTACCGCTT	TGAGTGAGCT	GATACCGCTC	GGCCGAGCCG	AACGACCGAG	CGCAGCCAGT	1980
CAGTGAGCGA	GGAAAGCGGAA	GAGCGCCAA	TACGCAAAC	GGCTCTCCC	GGCGCTTGGC	2040
CGATTCTTA	ATGCAGCTG	ATTAATGATT	ACATACGCT	CCGGTAGTA	GACCAGCAG	2100
CCGAGCCAGT	TCAGCGCTA	AAACGCCCTA	TACAATTAAG	CAGTAAAGA	AGTTAGAAC	2160
TACGCTAA	AAGCTACTTA	AAAATCGATC	TCGCAGTCCC	GATTGCCCTA	TCAAAACAG	2220
TTAAATCAA	CTGATTAAG	GTGCCAACG	AGCTATAAT	GATATAACAA	TATTAAGCA	2280
TTAATTAGAG	CAATATCAGG	CCGCCACGA	AAGGCAACTT	AAAAAGCGAA	ACCGCTCTAC	2340
TAACAGATT	ACTTTGAAA	AAGGCACATC	AGTATTAA	GCCGAATCC	TTATTAAGCG	2400
CCGAAATCAG	GCAGATAAAAG	CCATACAGGC	AGATAGACCT	CTACACTATTA	AATCGGCTTC	2460
TAGGCGCGCT	CCATCTAAAT	GTTCTGGCTG	TGGTGTACAG	GGGCATAAAA	TTACGCACTA	2520
CCCGAATCGA	TAGAACTACT	CATTTTATA	TAGAAGTCAG	AATTCTAGT	GTTTTGATCA	2580
TTTTAAATTT	TTATATGGCG	GGTGGTGGGC	AACTCGCTG	CGCGGCAAC	TCGCTTACCG	2640
ATTACGTTAG	GGCTGATATT	TACGTAAAAA	TCGTCAAGGG	ATGCAAGACCC	AAAGTAGTAA	2700
AACCCCCGGA	GTCAACAGCA	TCCAAGCCCA	AGTCCTTCAC	GGAGAAACCC	CAGCGTCCAC	2760
ATCACGAGCG	AAGGACCAAC	TCTAGGCATC	GGACGCACCA	TCCAATTAGA	AGCAGCAAAG	2820
CGAAACAGCC	CAAGAAAAG	GTCCGGCCGT	CGGCCCTTTC	TGCAACGCTG	ATCACGGCA	2880
GCGATCCAAC	CAACACCCCTC	CAGAGTGA	AGGGCGGAA	ATTTAAAGGG	ATTAATTCC	2940
ACTCAACCAC	AAATCACAGT	CGTCCCCGGT	ATTGTCCTG	AGAATGCAAT	TTAAACTCTT	3000
CTGCGAATCG	CTTGGATTCC	CCGCCCCTAG	TCGTAGAGCT	TAAAGTATGT	CCCTTGTCGA	3060
TGCGATGTAT	CACAACATAT	AAATACTAGC	AAGGGATGCC	ATGCTTGGAG	TTTCCAACTC	3120
AATTACCTC	TATCCACACT	TCTCTCCCT	CCTCAATCCT	CTATATACAC	AACTGGGAT	3180
CCTCACAC	ATG TTG GGC	GTC CGC CGT	CTA GGC	CTA GGC	GCC CTT GCT	3229
Met	Leu	Gly	Val	Val	Arg	Arg
1	5	10				
GCC	GCA	GCT	CTG	TCT	CTC	GGC
Ala	Ala	Ala	Leu	Ser	Ser	Leu
15	20	25	30			
ATT	CGG	TCT	CTC	GAG	GAA	CGT
Ile	Arg	Ser	Leu	Glu	Glu	Arg
35	40	45				
TGT	CAC	TTC	ATG	ATT	GGT	ATT
Cys	His	Phe	Met	Ile	Gly	Ile
50	55	60				
TAT	GAT	GAT	GAC	ATG	CAA	CGT
Tyr	Asp	Asp	Asp	Met	Gln	Arg
65	70	75				
GCT	CTG	AAC	ATC	GGC	GTT	GAC
Ala	Leu	Asn	Ile	Gly	Val	Asp
80	85	90				
GCC	TAT	GAC	TCT	GCC	GAC	CGT
Ala	Tyr	Asp	Ser	Ala	Asp	Arg
95	100	105	110			
GAT	TTC	AAC	TGG	TGG	AGC	CCC
Asp	Phe	Asn	Trp	Trp	Ser	Pro
115	120	125				
ATT	GCG	CAG	TAT	GCC	AGC	CGT
Ile	Ala	Gln	Tyr	Ala	Ser	Arg
130	135	140				
CCA	TTC	GCC	TCT	TCC	GCT	GGT
Pro	Phe	Ala	Ser	Ser	Phe	Ala
145	150	155				
CGC	TCT	GCT	GCA	GGC	TCC	AAC
Arg	Ser	Ala	Ala	AAC	AAC	TTC
160	165	170				
GGT	CAA	TCT	TCC	CCC	AAC	TGG
Gly	Gln	Ser	Ser	Pro	Ser	ATG
175	180	185	190			
TGG	GAT	AAT	GAT	GGA	AAC	AAG
Trp	Asp	Asn	Asp	Gly	Asn	Asn
195	200	205				
ACG	GTG	GCA	GAC	GGT	GAC	GCT
Thr	Val	Ala	Asp	Gly	Asp	Asn
210	215	220				

CCT TAC CTA GCG CCT GTC TCC CCT TGG TTT TTC ACC CAT TTT GGC CCT	3901
Pro Tyr Leu Ala Pro Val Ser Pro Trp Phe Phe Thr His Phe Gly Pro	
225 230 235	
GAA GTT TCA TAT TCC AAG AAC TGG GTC TTC CCA GGT GGT CCT CTG ATC	3949
Glu Val Ser Tyr Ser Lys Asn Trp Val Phe Pro Gly Gly Pro Leu Ile	
240 245 250	
TAT AAC CGG TGG CAA CAG GTC TTG CAG CAG GGC TTC CCC ATG GTT GAG	3997
Tyr Asn Arg Trp Gln Gln Val Leu Gln Gln Gly Phe Pro Met Val Glu	
255 260 265 270	
ATT GTT ACC TGG AAT GAC TAC GGC GAG TCT CAC TAC GTC GGT CCT CTG	4045
Ile Val Thr Trp Asn Asp Tyr Gly Glu Ser His Tyr Val Gly Pro Leu	
275 280 285	
AAG TCT AAG CAT TTC GAT GAT GGC AAC TCC AAA TGG GTC AAT GAT ATG	4093
Lys Ser Lys His Phe Asp Asp Gly Asn Ser Lys Trp Val Asn Asp Met	
290 295 300	
CCC CAT GAT GGA TTC TTG GAT CTT TCA AAG CCG TTT ATT GCT GCA TAT	4141
Pro His Asp Gly Phe Leu Asp Leu Ser Lys Pro Phe Ile Ala Ala Tyr	
305 310 315	
AAG AAC AGG GAT ACT GAT ATA TCT AAG TAT GTT CAA AAT GAG CAG CTT	4189
Lys Asn Arg Asp Thr Asp Ile Ser Lys Tyr Val Gln Asn Glu Gln Leu	
320 325 330	
GTT TAC TGG TAC CGC CGC AAC TTG AAG GCA TTG GAC TGC GAC GCC ACC	4237
Val Tyr Trp Tyr Arg Arg Asn Leu Lys Ala Leu Asp Cys Asp Ala Thr	
335 340 345 350	
GAC ACC ACC TCT AAC CGC CCG GCT AAT AAC GGA AGT GGC AAT TAC TTT	4285
Asp Thr Thr Ser Asn Arg Pro Ala Asn Asn Gly Ser Gly Asn Tyr Phe	
355 360 365	
ATG GGA CGC CCT GAT GGT TGG CAA ACT ATG GAT GAT ACC GTT TAT GTT	4333
Met Gly Arg Pro Asp Gly Trp Gln Thr Met Asp Asp Thr Val Tyr Val	
370 375 380	
GCC GCA CTT CTC AAG ACC GCC GGT AGC GTC ACG GTC ACG TCT GGC GGC	4381
Ala Ala Leu Leu Lys Thr Ala Gly Ser Val Thr Val Thr Ser Gly Gly	
385 390 395	
ACC ACT CAA ACG TTC CAG GCC AAC GCC GGA GCC AAC CTC TTC CAA ATC	4429
Thr Thr Gln Thr Phe Gln Ala Asn Ala Gly Ala Asn Leu Phe Gln Ile	
400 405 410	
CCT GCC AGC ATC GGC CAG CAA AAG TTT GCT CTA ACT CGC AAC GGT CAG	4477
Pro Ala Ser Ile Gly Gln Gln Lys Phe Ala Leu Thr Arg Asn Gly Gln	
415 420 425 430	
ACC GTC TTT AGC GGA ACC TCA TTG ATG GAT ATC ACC AAC GTT TGC TCT	4525
Thr Val Phe Ser Gly Thr Ser Leu Met Asp Ile Thr Asn Val Cys Ser	
435 440 445	
TGC GGT ATC TAC AAT TTC AAC CCA TAT GTT GGC ACC ATT CCT GCC GGC	4573
Cys Gly Ile Tyr Asn Phe Asn Pro Tyr Val Gly Thr Ile Pro Ala Gly	
450 455 460	
TTT GAC GAC CCT CTT CAG GCT GAC GGT CTT TTC TCT TTG ACC ATC GGA	4621
Phe Asp Asp Pro Leu Gln Ala Asp Gly Leu Phe Ser Leu Thr Ile Gly	
465 470 475	
TTG CAT GTC ACG ACT TGT CAG GCC AAG CCA TCT CTT GGA ACC AAC CCT	4669
Leu His Val Thr Thr Cys Gln Ala Lys Pro Ser Leu Gly Thr Asn Pro	
480 485 490	
CCT GTC ACT TCT GGC CCT GTG TCC TCG CTG CCA GCT TCC TCC ACC ACC	4717
Pro Val Thr Ser Gly Pro Val Ser Ser Leu Pro Ala Ser Ser Thr Thr	
495 500 505 510	
CGC GCA TCC TCG CCT GTT TCT TCA ACT CGT GTC TCT TCT CCC CCT	4765
Arg Ala Ser Ser Pro Pro Val Ser Ser Thr Arg Val Ser Ser Pro Pro	
515 520 525	
GTC TCT TCC CCT CCA GTT TCT CGC ACC TCT TCT CCC CCT CCC CCT CCG	4813
Val Ser Ser Pro Pro Val Ser Arg Thr Ser Ser Pro Pro Pro Pro Pro	
530 535 540	
GCC AGC AGC ACG CCG CCA TCG GGT CAG GTT TGC GTT GCC GGC ACC GTT	4861
Ala Ser Ser Thr Pro Pro Ser Gly Gln Val Cys Val Ala Gly Thr Val	
545 550 555	
GCT GAC GGC GAG TCC GGC AAC TAC ATC GGC CTG TGC CAA TTC AGC TGC	4909
Ala Asp Gly Glu Ser Gly Asn Tyr Ile Gly Leu Cys Gln Phe Ser Cys	
560 565 570	
AAC TAC GGT TAC TGT CCA CCG GGA CCG TGT AAG TGC ACC GCC TTT GGT	4957

Asn	Tyr	Gly	Tyr	Cys	Pro	Pro	Gly	Pro	Cys	Lys	Cys	Thr	Ala	Phe	Gly
575				580						585					590
GCT	CCC	ATC	TCG	CCA	CCG	GCA	AGC	AAT	GGG	CGC	AAC	GGC	TGC	CCT	CTA
Ala	Pro	Ile	Ser	Pro	Pro	Ala	Ser	Asn	Gly	Arg	Asn	Gly	Cys	Pro	Leu
				595					600						605
CCG	GGA	GAA	GGC	GAT	GGT	TAT	CTG	GGC	CTG	TGC	AGT	TTC	AGT	TGT	AAC
Pro	Gly	Glu	Gly	Asp	Gly	Tyr	Leu	Gly	Leu	Cys	Ser	Phe	Ser	Cys	Asn
				610				615				620			5053
CAT	AAT	TAC	TGC	CCG	CCA	ACG	GCA	TGC	CAA	TAC	TGT	TAG	TCTAGAGGGT		5102
His	Asn	Tyr	Cys	Pro	Pro	Thr	Ala	Cys	Gln	Tyr	Cys	*			
				625			630				635				
GA	CTG	GAC	ACC	CC	GG	GGT	TAG	GA	CA	AT	TC	GT	TAT	AG	GGG
GG	CA	AT	TT	GG	T	T	T	AT	AT	TC	AT	GT	G	AA	GG
CA	AG	T	C	AT	GT	T	G	AT	TC	GG	AT	GT	T	AA	AT
GA	AA	GG	CC	AT	GT	TT	CC	GT	GA	CC	GA	TC	CT	AC	AC
AC	AA	AG	AC	AT	GG	TT	CC	GT	AG	AC	AG	CT	CT	AC	CG
AT	TC	AT	GT	CA	TC	TT	CC	TC	TC	CT	CT	GT	GT	CT	CT
CA	AG	TT	GG	AG	CC	AT	CC	TC	TC	CT	CT	GT	GT	CT	CT
CA	AG	GG	GG	AG	CC	AC	CC	TC	TC	CT	CT	GT	GT	CT	CT
CA	AG	AG	GT	TAT	CT	CT	AC	TC	TC	CT	CT	GT	GT	CT	CT
TC	AA	AG	GT	TAT	CT	CT	AC	TC	TC	CT	CT	GT	GT	CT	CT
TC	AA	AG	GT	TAT	CT	CT	AC	TC	TC	CT	CT	GT	GT	CT	CT
AA	AG	GG	GT	TAT	CT	CT	AC	TC	TC	CT	CT	GT	GT	CT	CT
TT	AG	GG	GT	TAT	CT	CT	AC	TC	TC	CT	CT	GT	GT	CT	CT
TG	CC	CAT	CT	GC	CA	CT	AA	AT	TC	CC	AC	CG	CG	CC	CT
GC	CG	GG	CG	TC	AG	TT	CA	TC	TC	CT	AC	GG	GG	CT	CT
AT	CT	GT	GC	GG	TAT	TC	AC	AC	TC	TC	AT	GT	GT	CT	CT
CA	AT	GT	AA	AG	TC	TC	CC	CC	TC	TC	AT	CT	CT	AC	AC
TG	CT	CC	GG	GC	TC	TC	TT	AC	TC	TC	AT	CT	CT	AC	AC
GG	TT	TC	AC	CC	AA	AC	CC	CC	TC	TC	AT	CT	CT	AC	AC

PATENT CLAIMS

1. A method for constructing an expression vector comprising a mutanase gene obtained from a filamentous fungus suitable for heterologous production comprising the steps of:

- 5 a) isolating a DNA sequence encoding a mutanase from a filamentous fungus,
- b) introducing a kex2 site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the mutanase, or replacing the mutanase (pre)pro-sequence with a 10 (pre)pro-sequence comprising a kex2 or kex2-like site of another fungal enzyme,
- c) cloning the DNA sequence obtained in step b) into a suitable expression vector.

15 2. The method according to claim 1, wherein the mutanase is obtained from the genus *Trichoderma*, preferably a strain of the species *T. harzianum*, especially the strain *T. harzianum* CBS 243.71.

20 3. The method according to claim 2, in which the mutanase DNA sequence is isolated from or produced on the basis of a nucleic acid library of *Trichoderma harzianum* CBS 243.71.

4. The method according to any of claims 1 to 3, wherein the 25 mutanase (pre)pro-sequence is replaced by the Lipolase® (pre)pro-sequence or the TAKA-amylase (pre)pro-sequence.

5. An expression vector comprising a mutanase gene and a DNA sequence encoding a pro-peptide with a kex2 site or kex2-like 30 site between the DNA sequences encoding said pro-peptide and the mature region of the mutanase.

6. The expression vector according to claim 5, further comprising an operably linked promoter sequence and/or a prepro- 35 sequence.

7. The expression vector according to claims 5 and 6, wherein the prepro-sequence comprise the original mutanase signal sequence, or the Lipolase® signal-sequence, or the TAKA pro-sequence and the original mutanase pro-sequence with a kex2 or 5 kx2-like site, or the Lipolase® pro-sequence, or the TAKA pro-sequence.

8. The expression vector according to claim 7, wherein the promoter is the TAKA promoter or TAKA:TPI promoter.

10

9. The expression vector according to any claims 5 to 8, being the vector pMT1796.

10. A filamentous host cell for production of recombinant 15 mutanase derived from a filamentous fungus being from the genus *Trichoderma*, such as a strain of *T. harzianum*, or the genus *Aspergillus*, such as a strain of *A. oryzae* or *A. niger*, or a strain of the genus *Fusarium*, such as a strain of *Fusarium oxyphorium*, *Fusarium graminearum*, *Fusarium sulphureum*, *Fusarium 20 cerealis*.

11. The host cell according to claim 10 wherein the host cell is a protease deficient of protease minus strain.

12. The host cell according to claim 11, wherein the host cell 25 is the protease deficient strain *Aspergillus oryzae* JaL125 having the alkaline protease gene named "alp" deleted.

13. A process for producing a recombinant mutanase in a host 30 cell, comprising the steps:

- a) transforming an expression vector comprising a mutanase gene with a kex2 site or kex2-like site between the DNA sequences encoding the pro-peptide and the mature region of the mutanase into a suitable filamentous fungus host cell,
- 35 b) cultivating the host cell in a suitable culture medium under conditions permitting expression and secretion of an active mutanase,

c) recovering and optionally purifying the secreted active recombinant mutanase from the culture medium.

14. The process according to claim 13 wherein the recombinant expression vector is prepared according to the method of claim 1 to 4.

15. The process according to claim 13 and 14, wherein the filamentous host is a host cell according to any of claims 7 to 10 9.

16. An isolated recombinant mutanase produced according to the process according to any of claims 13 to 15.

15 17. A substantially pure wild-type mutanase obtained from *Trichoderma harzianum* CBS 243.71 essentially free of any contaminants.

18. A composition comprising a recombinant mutanase according 20 to claim 16 or a substantially pure wild-type mutanase according to claim 17 and further other ingredients conventionally used in food, feed and/or pet food products.

19. An oral care composition comprising a recombinant mutanase 25 according to claim 16 or a substantially pure wild-type mutanase according to claim 17, further comprising an enzyme selected from the group of dextranases, oxidases, peroxidases, haloperoxidases, laccases, proteases, endoglucosidases, lipases, amylases, and mixtures thereof.

30

20. An oral care product comprising a recombinant mutanase according to claim 16 or a substantially purified mutanase according to claim 17 or an oral care composition according to claim 19 and further comprising ingredients conventionally used 35 in oral care products.

21. The oral care product according to claim 20, being a dentifrice, such as a toothpaste, tooth powder or a mouth wash.
22. Use of the recombinant mutanase according to claim 16 or the substantially purified mutanase according to claim 17 or an oral care composition of claim 19 or oral care product according to claims 20 and 21 for preventing the formation of dental plaque or removing dental plaque.
- 10 23. The use of the recombinant mutanase according to claims 16 or the substantially purified mutanase according to claim 17 or a oral care composition of claim 19 or oral care product according to claims 18 and 20 in oral care products for humans and/or animals.
- 15 24. Use of the composition according to claim 18, in food, feed and/or pet food products.

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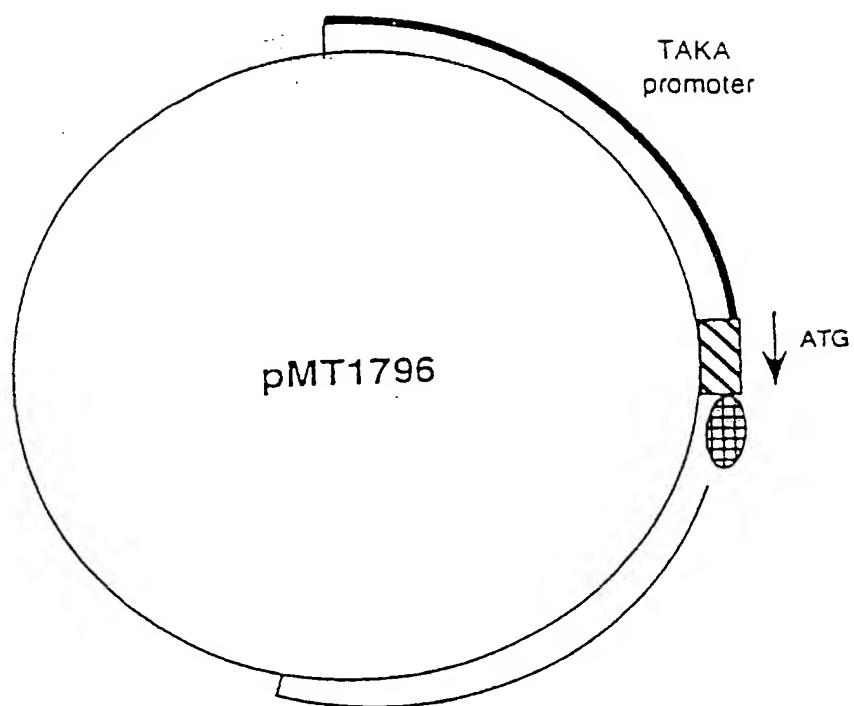


Fig. 1

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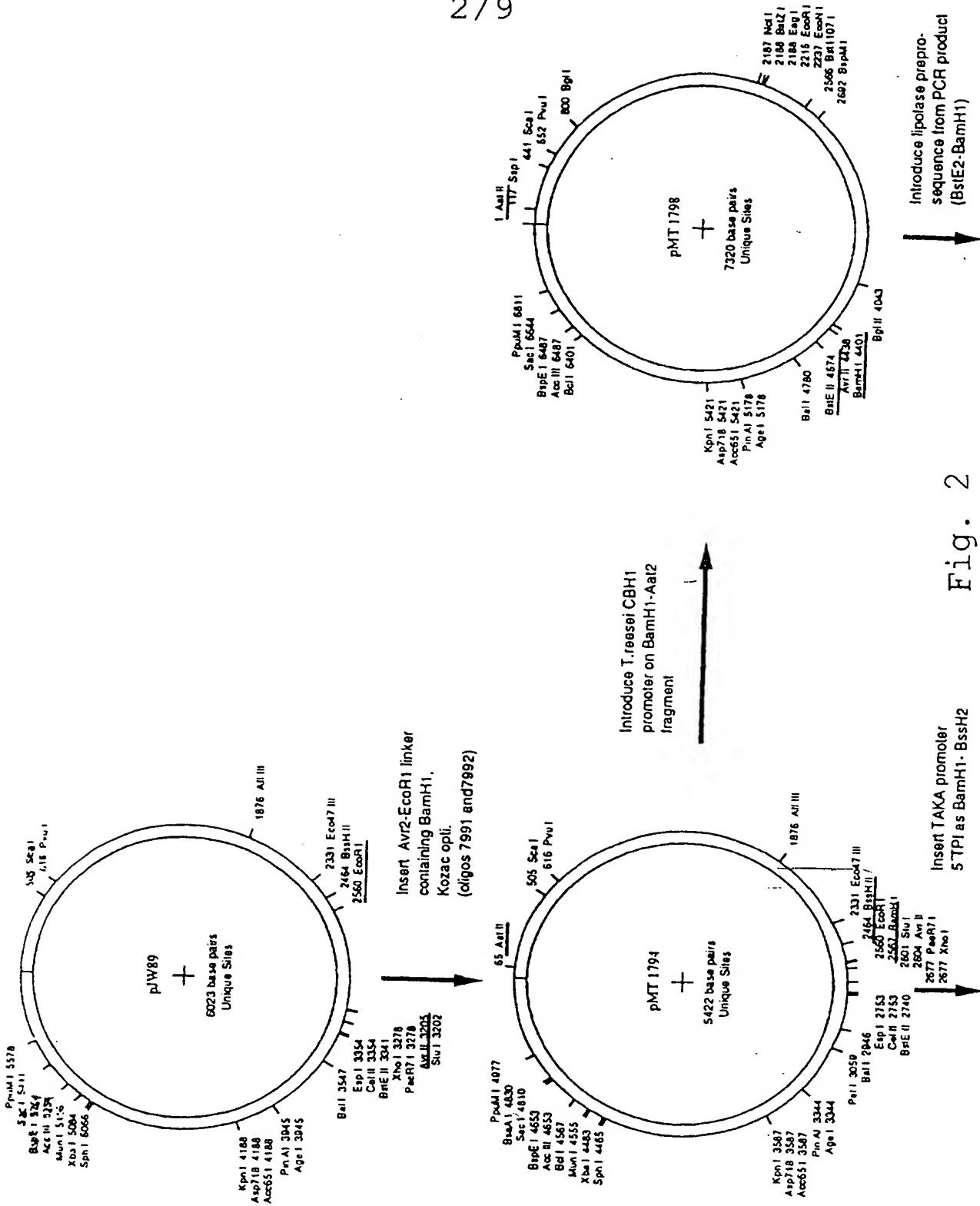
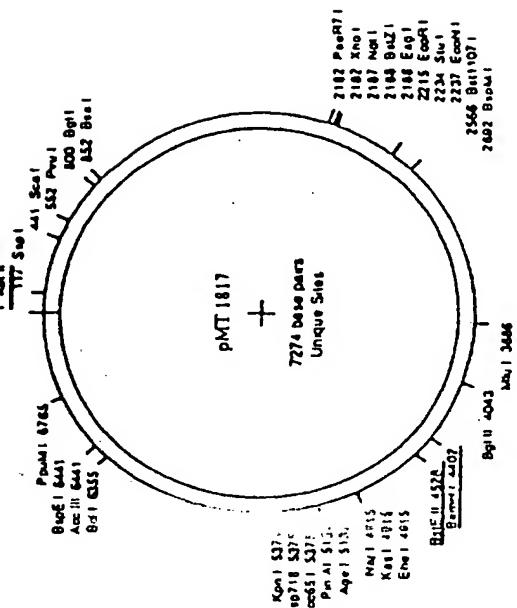
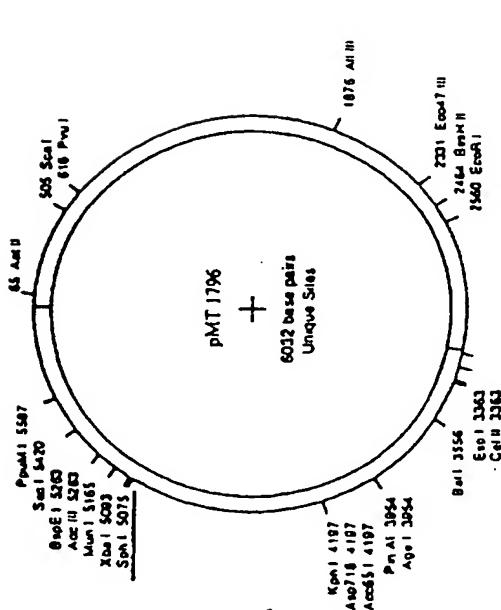
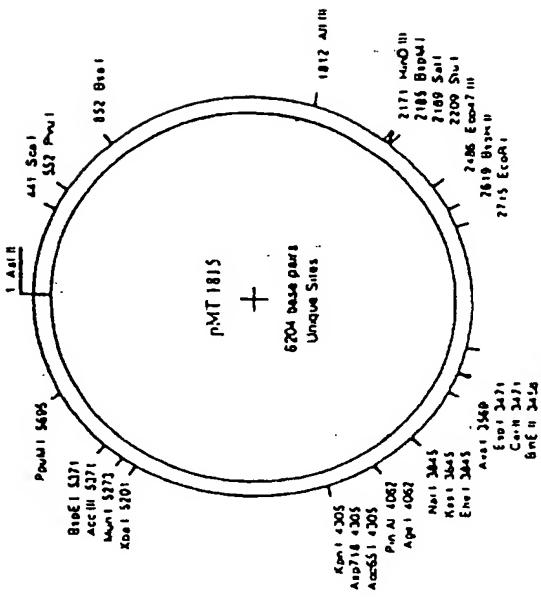


Fig. 2

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Shift promoter back to
TAKA 5' TPI
(AaII - BamH1)



Insert mutanase gene w/out
KEK2 site;
XbaI-SphI from pW74

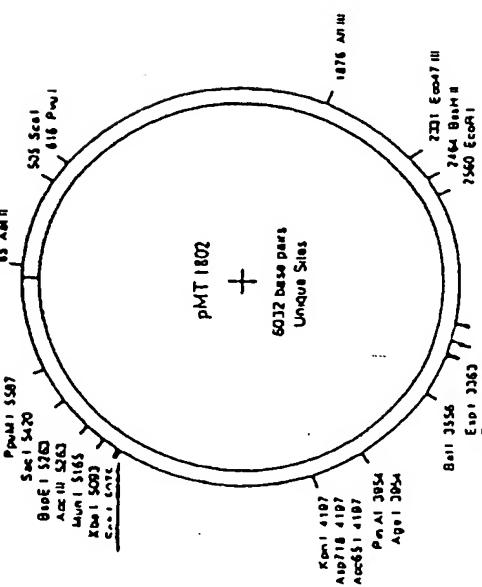
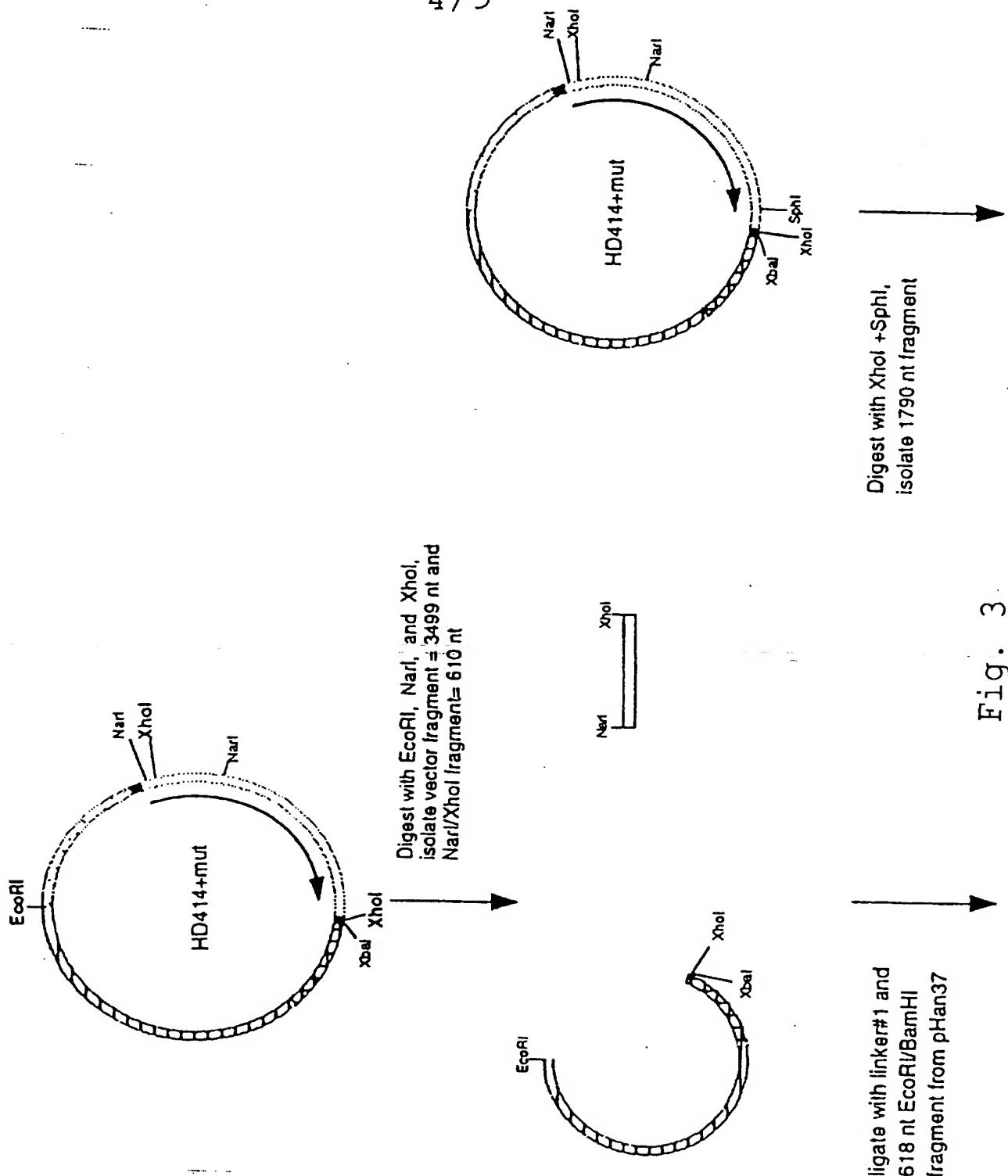


Fig. 2

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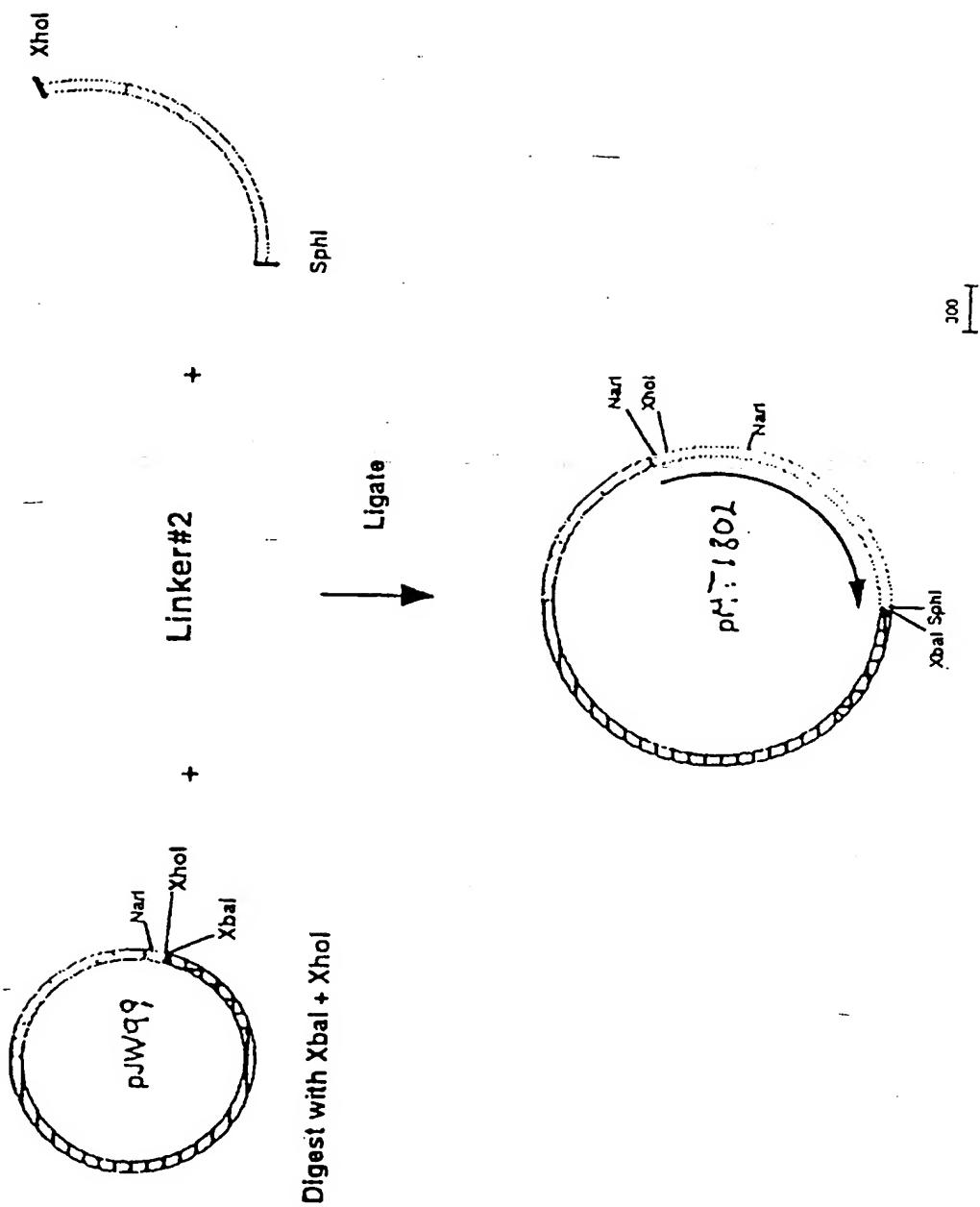


Fig. 3

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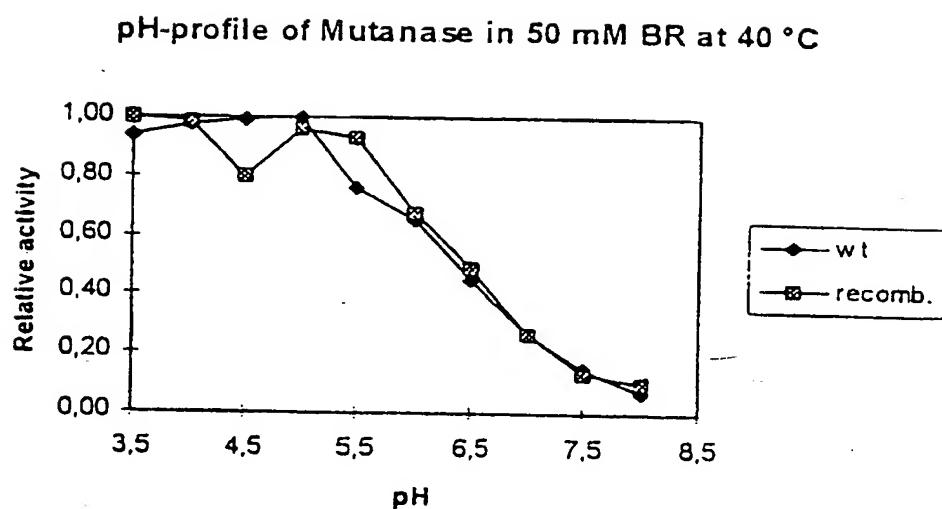


Fig. 4

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Temperature-profile of Mutanase in 0.1 M sodium phosphate, pH 7

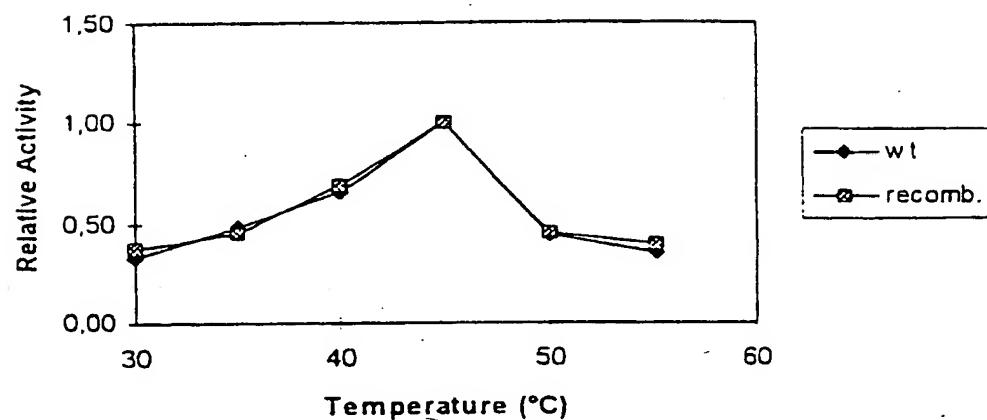


Fig. 5

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Temperature Stability of Mutanase in 0.1 M sodium phosphate, pH 7

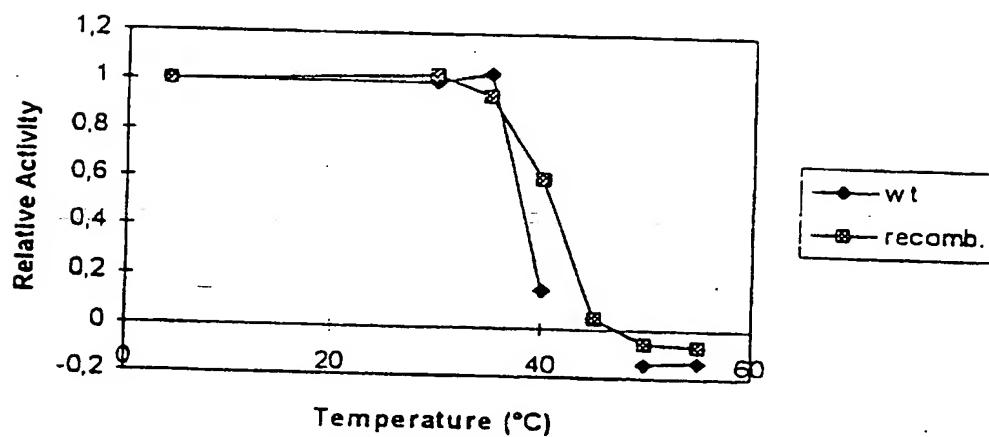


Fig. 6

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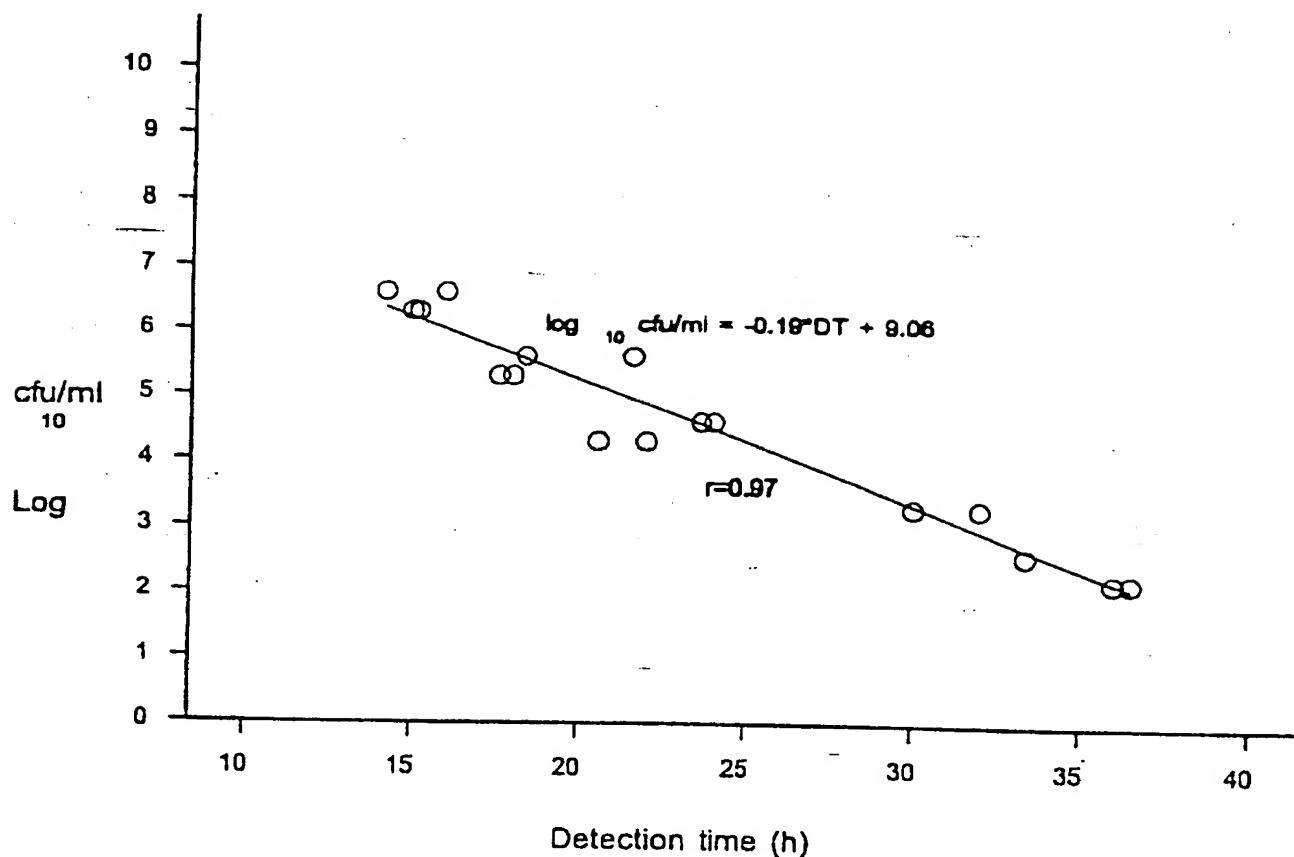


Fig. 7

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